

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2005, 19:23:54 ; Search time 167 Seconds
(without alignments)
83.373 Million cell updates/sec

Title: US-09-809-060A-1

Perfect score: 195

Sequence: 1 YTSLSHSLIESQNOQEKNEQELLDKWLNLWNWF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	195	100.0	36	2	AAR64364 DP-178 de
2	195	100.0	36	2	AAR98398 DP178 cor
3	195	100.0	36	2	AAW17011 HIV-1 der
4	195	100.0	36	2	AAW22912 SEQ ID NO
5	195	100.0	36	2	AAW22805 SEQ ID NO
6	195	100.0	36	2	AAW31974 HIV-1 LAI
7	195	100.0	36	2	AAW31955 Synthetic
8	195	100.0	36	3	AAW89999 Core poly
9	195	100.0	36	3	AAW8665 Core poly
10	195	100.0	36	3	AAW8777 Core poly
11	195	100.0	36	3	AAW8982 Core poly
12	195	100.0	36	3	AAW89424 Core poly
13	195	100.0	36	3	AAW89692 Core poly
14	195	100.0	36	3	AAW89242 Core poly
15	195	100.0	36	3	AAW89883 Core poly
16	195	100.0	36	3	AAW88722 Core poly
17	195	100.0	36	3	AAW88135 Core poly
18	195	100.0	36	3	AAW89136 Core poly
19	195	100.0	36	3	AAW89735 Core poly
20	195	100.0	36	3	AAW14533 HIV-1 iso
21	195	100.0	36	3	AAW52818 T20/DP178
22	195	100.0	36	3	AAW52655 T20/DP178
23	195	100.0	36	3	AAW52688 T20/DP178
24	195	100.0	36	4	AAW65861 Amino aci
25	195	100.0	36	4	AAW54784 HIV antiv

26	195	100.0	36	4	AAW54902 Anti-HIV
27	195	100.0	36	4	AAW54935 Anti-HIV
28	195	100.0	36	4	AAW92243 Virus rel
29	195	100.0	36	4	AAW92352 Virus rel
30	195	100.0	36	4	AAW77083 Core poly
31	195	100.0	36	4	AAW78136 Core poly
32	195	100.0	36	4	AAW78400 Core poly
33	195	100.0	36	4	AAW77595 Core poly
34	195	100.0	36	4	AAW77020 Core poly
35	195	100.0	36	4	AAW77084 Core poly
36	195	100.0	36	4	AAW77622 Core poly
37	195	100.0	36	4	AAW77623 Core poly
38	195	100.0	36	4	AAW78178 Core poly
39	195	100.0	36	4	AAW77490 Core poly
40	195	100.0	36	4	AAW78384 Core poly
41	195	100.0	36	4	AAW77491 Core poly
42	195	100.0	36	4	AAW77621 Core poly
43	195	100.0	36	4	AAW78383 Core poly
44	195	100.0	36	4	AAW77825 Core poly
45	195	100.0	36	4	AAW78093 Core poly

ALIGNMENTS

RESULT 1	AAW64364	standard; peptide; 36 AA.
AC	AAW64364;	
DT	25-MAR-2003 (revised)	
DT	24-AUG-1995 (first entry)	
XX	DP-178 derived from HIV-1 isolate LAI has antiviral activity.	
XX	antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;	
XX	human immunodeficiency virus; transmembrane protein; gp41; alpha helix;	
KW	leucine zipper; DP-185.	
XX	Synthetic.	
OS		
XX	Key	Location/Qualifiers
FT	Modified-site	1
FT		/note="optionally has an amino, acetyl, 9-
FT		fluorenylmethoxy-carbonyl, hydrophobic or macromolecular
FT		carrier gp. attached"
FT	Modified-site	38
FT		/note="optionally has a carboxyl, amido, hydrophobic or
FT		macromolecular carrier gp. attached"
PN	W09428920-AI.	
XX	22-DEC-1994.	
PD		
XX	07-JUN-1994; 94MO-US005739.	
PF		
XX	07-JUN-1993; 93US-00073028.	
PR		
XX	(UYDU-) UNIV DUKE.	
PA		
XX	Bolognesi DP, Matthews TV, Wild CT, Barney SO, Lambert DM;	
XX	Petteaway SR;	
DR	WPI, 1995-036105/05.	
XX		
XX	Computer search generated synthetic peptides - are inhibitors of HIV	
PT	transmission.	
PS	Claim 11; Page 132; 182pp; English.	
XX	AAW64364 is designated DP-178, and corresponds to amino acids 638 to 673	
CC	of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative	

CC alpha helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a leucine
 CC zipper motif. The peptides complex via non-covalent protein-protein
 CC interactions, and possess anti-viral activity. Homologues of these
 CC peptides were identified by a computer assisted peptide sequence search.
 CC The peptides inhibit transmission to uninfected cells, and can also be
 CC used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR
 CC -2003 to correct PN field.)

XX Sequence 36 AA;

Query Match 100.0%; Score 195; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLHSLIESQNOQEKNEQELLELDKWSLIMNMF 36
 DB 1 YTSLSLHSLIESQNOQEKNEQELLELDKWSLIMNMF 36

RESULT 2
 AAR98398

ID AAR98398 standard; peptide; 36 AA.

AC AAR98398;

DT 16-OCT-2003 (revised)
 DT 17-FEB-1997 (first entry)

DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.

KW Antifusogenic activity; antiviral capability; coiled-coil peptide;
 KM ALuMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KM Influenza virus; hepatitis B virus.

OS Human immunodeficiency virus 1.

XX WO9619495-A1.

PD 27-JUN-1996.

PF 20-DEC-1995; 95WO-US016733.

PR 20-DEC-1994; 94US-00360107.
 PR 06-JUN-1995; 95US-00470896.

PA (UYDU-) UNIV DUKE.

PA (TRIM-) TRIMERIS INC.

PI Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;
 PI Peteway SR, Langlois AJ;

DR WPI; 1996-309517/31.

PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 PT isolated peptide recognised by an ALuMOT15, 107x178x4 or PLZIP sequence
 PT search motif.

PS Disclosure: Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit
 CC antifusogenic activity, antiviral capability and/or the ability to
 CC modulate intracellular processes involving coiled-coil peptide
 CC structures. These peptides are recognised by the ALuMOT15, 107x178x4 and
 CC PLZIP search motifs. These peptides may be used to inhibit the
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 195; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLHSLIESQNOQEKNEQELLELDKWSLIMNMF 36
 DB 1 YTSLSLHSLIESQNOQEKNEQELLELDKWSLIMNMF 36

RESULT 3
 AAM17011

ID AAM17011 standard; peptide; 36 AA.

AC AAM17011;

DT 17-OCT-2003 (revised)
 DT 30-JUN-1997 (first entry)

DE HIV-1 derived peptide useful for treatment of HIV infection.

KW HIV; STV; human; simian immunodeficiency virus; glycoprotein 41;
 KM Transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;
 KM replication; transmission.

OS Human immunodeficiency virus 1; LAI isolate.

PN WO9640191-A1.

PD 19-DEC-1996.

PF 06-JUN-1996; 96WO-US009499.

PR 07-JUN-1995; 95US-00481957.

PA (TRIM-) TRIMERIS INC.

PI Johnson RM, Lambert DM;

DR WPI; 1997-099886/09.

PT Compsns. contg. DP-178 or DP-107 in combination with other therapeutic
 PT agent - useful for treatment of HIV infection, esp. by inhibiting
 PT replication or transmission of HIV.

PS Claim 2; Fig 1; 84pp; English.

CC AAM17011 represents a peptide designated DP-178, a peptide derived from
 CC HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The peptide
 CC corresponds to residues 638-673 of gp41. DP-178 and its derivatives are
 CC used in combination with a therapeutic agent, e.g. a reverse
 CC transcriptase, viral protease, cyclokin, glycosylation or viral RNA
 CC processing inhibitor or a nucleoside inhibitor. The peptides work by
 CC inhibiting viral replication or inhibiting transmission. They may also be
 CC used in vaccines for protecting against HIV infection. (Updated on 17-OCT
 CC -2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 195; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLHSLIESQNOQEKNEQELLELDKWSLIMNMF 36
 DB 1 YTSLSLHSLIESQNOQEKNEQELLELDKWSLIMNMF 36

RESULT 4
 AAY22912

ID AAY22912 standard; peptide; 36 AA.

AC AAY22912;

DT 19-AUG-1999 (first entry)

DE SEQ ID NO. 108 from WO9820036.

XX HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
 KM antibody; viral membrane fusion; viral infectivity;
 KM ligand affinity purification; protein A replacement;
 KM immunoglobulin purification; epitope mimic.
 XX Human immunodeficiency virus.
 OS
 XX WO9820036-A1.
 PN
 XX 14-MAY-1998.
 PD
 XX 05-NOV-1997; 97WO-US020069.
 PF
 XX 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-00876698.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 PI Wells JA;
 DR WPI; 1998-286866/25.
 XX
 XX Production of constrained helical peptide(s) by linking side chains on
 PT termini of octa:peptide - derived from human immunodeficiency virus gp41
 PT protein, useful in vaccines for treatment and prevention of infection.
 XX
 XX Disclosure; Page 233-234; 279pp; English.
 PS
 XX Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
 CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
 CC AAY22903 represent consensus sequences of various sections of the gp41
 CC protein). Sequences derived from the peptides are used to produce
 CC constrained helical peptides of the invention. The constrained helical
 CC peptide is produced by synthesizing an octapeptide in which both terminal
 CC amino acids have a side-chain that includes a group able to form an amide
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification); as
 CC epitope mimics for antibody production; for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 CC
 XX
 SQ Sequence 36 AA;
 QY
 Db 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36
 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36

RESULT 5
 AAY22805
 ID AAY22805 standard; peptide; 36 AA.
 XX
 AC AAY22805;
 XX
 DT 19-AUG-1999 (first entry)
 XX
 DE SEQ ID NO. 1 from WO9820036.
 XX

KM HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
 KM antibody; viral membrane fusion; viral infectivity;
 KM ligand affinity purification; protein A replacement;
 KM immunoglobulin purification; epitope mimic.
 XX Human immunodeficiency virus.
 OS
 XX WO9820036-A1.
 PN
 XX 14-MAY-1998.
 PD
 XX 05-NOV-1997; 97WO-US020069.
 PF
 XX 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-00876698.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 PI Wells JA;
 DR WPI; 1998-286866/25.
 XX
 XX Production of constrained helical peptide(s) by linking side chains on
 PT termini of octa:peptide - derived from human immunodeficiency virus gp41
 PT protein, useful in vaccines for treatment and prevention of infection.
 XX
 XX Disclosure; Page 143-144; 279pp; English.
 PS
 XX Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
 CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
 CC AAY22903 represent consensus sequences of various sections of the gp41
 CC protein). Sequences derived from the peptides are used to produce
 CC constrained helical peptides of the invention. The constrained helical
 CC peptide is produced by synthesizing an octapeptide in which both terminal
 CC amino acids have a side-chain that includes a group able to form an amide
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification); as
 CC epitope mimics for antibody production; for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 CC
 XX
 SQ Sequence 36 AA;
 QY
 Db 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36
 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36

RESULT 6
 AAY1974
 ID AAY1974 standard; peptide; 36 AA.
 XX
 AC AAY1974;
 XX
 DT 17-OCT-2003 (revised)
 DT 21-DEC-1999 (first entry)
 XX
 DE HIV-1 LAI gp41 T-20 peptide.
 XX

KM T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
 OS Human immunodeficiency virus 1.
 XX WO9948513-A1.
 XX 30-SEP-1999.
 PD 22-MAR-1999; 99WO-US006230.
 PF 23-MAR-1998; 98US-00045920.
 PR 01-MAY-1998; 98US-00071877.
 XX (TRIM-) TRIMERIS INC.
 PA Kang M, Bray B, Lichty M, Mader C, Merutka G;
 PI WPI; 1999-591038/50.
 DR Methods of peptide synthesis, particularly used to produce T-20 or T-20
 XX like peptides.
 PT Methods of peptide synthesis, particularly used to produce T-20 or T-20
 PS like peptides.
 XX Disclosure; Page 9; 120pp; English.
 CC The present sequence represents a peptide, designated T-20 (or DP-178),
 CC that corresponds to amino acids 638-673 of the transmembrane protein gp41
 CC of HIV-1 LAI isolate. The invention relates to methods for the synthesis
 CC of peptides, in particular C- and N-terminal modified T-20 (see AAY31955)
 CC and T-20-like peptides. The method involves synthesizing specific side-
 CC chain protected peptide fragment intermediates (see AAY31956-73) of T-20
 CC or a T-20-like peptide on a solid support, coupling the protected
 CC fragments in solution to form a protected T-20 or T-20-like peptide,
 CC followed by deprotection of the side chains to yield the final T-20 or T-
 CC 20-like peptide. The invention also relates to individual peptide
 CC fragments which act as intermediates in the synthesis of peptides of
 CC interest (e.g. T-20), and to particular groups of peptide fragments which
 CC act as intermediates in the synthesis of the peptide of interest. The
 CC method allows for the large scale, economical production of high purity
 CC peptides. (Updated on 17-Oct-2003 to standardise OS field)
 CC XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 195; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLIHSLIBESQNOQEKNEQELLEDKMASLMMNF 36
 DB 1 YTSLIHSLIBESQNOQEKNEQELLEDKMASLMMNF 36
 RESULT 7
 AAY31955
 ID AAY31955 standard; peptide; 36 AA.
 XX
 AC AAY31955;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Synthetic peptide T-20 (DP-178).
 XX
 KM T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 XX
 FT Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 36 /note= "C-terminal amide"
 FT /note= "C-terminal amide"
 XX
 PN WO9948513-A1.

XX 30-SEP-1999.
 PD 22-MAR-1999; 99WO-US006230.
 PF 23-MAR-1998; 98US-00045920.
 PR 01-MAY-1998; 98US-00071877.
 XX (TRIM-) TRIMERIS INC.
 PA Kang M, Bray B, Lichty M, Mader C, Merutka G;
 PI WPI; 1999-591038/50.
 DR Methods of peptide synthesis, particularly used to produce T-20 or T-20
 XX like peptides.
 PT Methods of peptide synthesis, particularly used to produce T-20 or T-20
 PS like peptides.
 XX Claim 1; Page 102; 120pp; English.
 CC The present sequence represents an N- and C-terminal modified peptide,
 CC designated T-20 (or DP-178), corresponding to amino acids 638-673 of the
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention relates to
 CC methods for the synthesis of peptides, in particular T-20 and T-20-like
 CC peptides. The method involves synthesizing specific side-chain protected
 CC peptide fragment intermediates of T-20 or a T-20-like peptide on a solid
 CC support, coupling the protected fragments in solution to form a protected
 CC T-20 or T-20-like peptide, followed by deprotection of the side chains to
 CC yield the final T-20 or T-20-like peptide. The invention also relates to
 CC individual peptide fragments (see AAY31956-73) which act as intermediates
 CC in the synthesis of peptides of interest (e.g. T-20), and to particular
 CC groups of peptide fragments which act as intermediates in the synthesis
 CC of the peptide of interest. The method allows for the large scale,
 CC economical production of high purity peptides
 CC XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 195; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLIHSLIBESQNOQEKNEQELLEDKMASLMMNF 36
 DB 1 YTSLIHSLIBESQNOQEKNEQELLEDKMASLMMNF 36
 RESULT 8
 AAY89999
 ID AAY89999 standard; peptide; 36 AA.
 XX
 AC AAY89999;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Core polypeptide fragment T No. 1598.
 XX
 KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiating factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 OS
 XX
 PN WO9959615-A1.
 PD 25-NOV-1999.
 PF 20-MAY-1999; 99WO-US011219.
 PR 20-MAY-1998; 98US-00082279.
 XX (TRIM-) TRIMERIS INC.
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 PI

XX
DR WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
PS Disclosure; Page 48; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY86651-Y9055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.8e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLEDKMSLWNMF 36
DB 1 YTSLSHSLIESQNOQEKNEQELLEDKMSLWNMF 36

RESULT 9
AAY8665 standard; peptide; 36 AA.
XX
AC AAY8665;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 20.
XX
KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN MO9959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
PS Disclosure; Page 21; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide

CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.8e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLEDKMSLWNMF 36
DB 1 YTSLSHSLIESQNOQEKNEQELLEDKMSLWNMF 36

RESULT 10
AAY89777 standard; peptide; 36 AA.
XX
AC AAY89777;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 1343.
XX
KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN MO9959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99WO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.
XX
PS Disclosure; Page 44; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 XX
 SQ Sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLHSLIESQNOEKNEQELLEDKWSLWNMF 36
 1 YTSLSLHSLIESQNOEKNEQELLEDKWSLWNMF 36

RESULT 11
 AAY89982
 ID AAY89982 standard; peptide; 36 AA.

AC AAY89982;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 1559.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

PN WO959615-A1.

XX 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties

PT comprises enhancer sequence.

PS Disclosure; Page 48; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide

CC sequence linked to core polypeptides. The enhancer polypeptides are

CC derived from various retroviral envelope (gp41) protein sequences,

CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the

CC pharmacokinetic properties such as increasing the half-life of any core

CC polypeptide that they are linked to. The core polypeptides are any

CC polypeptide that may be introduced into a living system and that can

CC function as a pharmacologically useful peptide for the treatment or

CC prevention of a disease. The core polypeptides are bioactive peptides

CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral

CC infection and can be used in anti-viral and anti-fusogenic treatments.

CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can

CC be used in the invention. Some sequences among those indicated also

CC comprise enhancer fragments at terminal ends and form hybrid polypeptides

XX Sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLHSLIESQNOEKNEQELLEDKWSLWNMF 36
 1 YTSLSLHSLIESQNOEKNEQELLEDKWSLWNMF 36

RESULT 12
 AAY89424
 ID AAY89424 standard; peptide; 36 AA.

AC AAY89424;
 DT 23-MAY-2000 (first entry)
 DE Core polypeptide fragment T No. 974.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

PN WO959615-A1.

XX 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties

PT comprises enhancer sequence.

PS Disclosure; Page 36; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide

CC sequence linked to core polypeptides. The enhancer polypeptides are

CC derived from various retroviral envelope (gp41) protein sequences,

CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the

CC pharmacokinetic properties such as increasing the half-life of any core

CC polypeptide that they are linked to. The core polypeptides are any

CC polypeptide that may be introduced into a living system and that can

CC function as a pharmacologically useful peptide for the treatment or

CC prevention of a disease. The core polypeptides are bioactive peptides

CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral

CC infection and can be used in anti-viral and anti-fusogenic treatments.

CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can

CC be used in the invention. Some sequences among those indicated also

CC comprise enhancer fragments at terminal ends and form hybrid polypeptides

XX Sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLHSLIESQNOEKNEQELLEDKWSLWNMF 36
 1 YTSLSLHSLIESQNOEKNEQELLEDKWSLWNMF 36

RESULT 13
 AAY89692 standard; peptide; 36 AA.
 AAY89692;
 23-MAY-2000 (first entry)
 Core polypeptide fragment T No. 1254.
 Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 anti-fusogenic; differentiation factor; interleukin; interferon;
 colony stimulating factor; hormone; angiogenic factor.
 Unidentified.
 OS
 XX MO9959615-A1.
 XX PN
 XX PD 25-NOV-1999.
 XX PF 20-MAY-1999; 99WO-US011219.
 XX PR 20-MAY-1998; 98US-00082279.
 XX PA (TRIM-) TRIMERIS INC.
 XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX DR WPI; 2000-136792/12.
 XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 XX PT comprises enhancer sequence.
 XX PS Disclosure; Page 42; 124pp; English.
 XX CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 195; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8, 8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36
 DB 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36
 RESULT 14
 AAY89242 standard; peptide; 36 AA.
 AAY89242;
 23-MAY-2000 (first entry)
 Core polypeptide fragment T No. 680.

XX
 KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 KM colony stimulating factor; hormone; angiogenic factor.
 OS
 XX Unidentified.
 XX OS
 XX PN MO9959615-A1.
 XX PD 25-NOV-1999.
 XX PF 20-MAY-1999; 99WO-US011219.
 XX PR 20-MAY-1998; 98US-00082279.
 XX PA (TRIM-) TRIMERIS INC.
 XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
 XX DR WPI; 2000-136792/12.
 XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 XX PT comprises enhancer sequence.
 XX PS Disclosure; Page 32; 124pp; English.
 XX CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
 CC factor. The peptides of the invention can be used for inhibiting viral
 CC infection and can be used in anti-viral and anti-fusogenic treatments.
 CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
 CC be used in the invention. Some sequences among those indicated also
 CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
 CC
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 195; DB 3; Length 36;
 Best Local Similarity 100.0%; Pred. No. 8, 8e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36
 DB 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36
 RESULT 15
 AAY89983 standard; peptide; 36 AA.
 AAY89983;
 23-MAY-2000 (first entry)
 Core polypeptide fragment T No. 1563.
 Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 anti-fusogenic; differentiation factor; interleukin; interferon;
 colony stimulating factor; hormone; angiogenic factor.
 OS
 XX Unidentified.
 XX OS
 XX PN MO9959615-A1.

XX 25-NOV-1999.
PD
XX
PF 20-MAY-1999; 99WO-US011219.
XX
XX
PR 20-MAY-1998; 98US-00082279.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI
XX WPI; 2000-136792/12.
DR
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
XX
PS Disclosure; Page 48; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AY88651-Y9055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.8e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEQLLELDKMASLNNWF 36
Db 1 YTSLSHSLIEESQNOQEKNEQLLELDKMASLNNWF 36

Search completed: September 20, 2005, 19:44:44
Job time : 169 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	195	100.0	851	2	S33985	env polyprotein - hum
2	195	100.0	854	2	S13288	env protein - hum
3	195	100.0	856	1	VCLJH3	env polyprotein p
4	195	100.0	861	1	VCLJH1	env polyprotein p
5	186	95.4	443	2	C41621	env polyprotein p
6	186	95.4	856	1	VCLJ3W	env polyprotein p
7	186	95.4	856	1	VCLJVL	env polyprotein p
8	186	95.4	861	1	VCLJSC	env polyprotein p
9	183	93.8	357	2	S21994	envelope protein
10	183	93.8	358	2	S21998	envelope protein
11	182	93.3	357	2	S21996	envelope protein
12	179	91.8	847	2	T09448	envelope glycopro
13	179	91.8	847	2	S13289	env protein - hum
14	178	91.3	445	2	A41621	env polyprotein M
15	177	90.8	358	2	S70417	envelope protein
16	177	90.8	358	2	S22000	envelope protein
17	177	90.8	358	2	S22002	envelope protein
18	177	90.8	852	2	T12016	envelope glycopro
19	177	90.8	855	1	VCLJDN	env polyprotein p
20	176	90.3	357	2	S22004	envelope protein
21	176	90.3	855	1	VCLJAJ	env polyprotein p
22	174	89.2	853	2	S54384	envelope polyprot
23	174	89.2	855	1	VCLJZR	env polyprotein p
24	173	88.7	357	2	S22006	envelope protein
25	173	88.7	843	1	H44001	env polyprotein p
26	172	88.2	846	1	VCLJND	env polyprotein p
27	170	87.2	357	2	S21992	envelope protein
28	170	87.2	852	1	VCLJBR	env polyprotein -
29	168	86.2	729	1	VCLJXK	env polyprotein p

30	168	86.2	86.1	1	VCJ4JB	env polyprotein p
31	167	85.6	85.9	2	T01672	envelope polyprote
32	164	84.1	45.4	2	B41621	env polyprotein D
33	163	83.6	86.8	1	VCJ4H4	env polyprotein -
34	160	82.1	136	2	JT0266	envelope polyprotee
35	160	82.1	136	2	JT0954	envelope polyprotee
36	151	77.4	85.4	1	VCJ4S1	env polyprotein pr
37	149	76.4	85.6	1	A44963	env polyprotein pr
38	147	75.4	35.7	2	S21990	envelope protein g
39	136	69.7	87.7	2	S4197	envelope protein p
40	119	61.0	86.3	2	A53034	gag polyprotein -
41	86	44.1	86.1	1	VCJ4J3	env polyprotein -
42	86	44.1	88.1	1	S03068	env protein - huma
43	85	43.1	88.9	1	VCJ4G5	env polyprotein -
44	85	43.6	151	2	S30451	env protein - huma
45	85	43.6	151	2	S30452	env protein - huma

ALIGNMENTS

RESULT 1

env polypolprotein human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R:Carlini, P.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CDR>
A:Cross-references: UNIREP:Q78243; EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C:Superfamily: type B retrovirus env polypolprotein

Query Match	100.0%;	Score 195;	DB 2;	Length 851;
Best Local Similarity	100.0%;	Pred. No. 2.3e-15;		
Matches	36;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY 1 YTSLIHSLIEESQNQEKNQELLEDKASLWVWF 36
| | | | | | | | | | | | | | | | | | | |
DB 633 YTSLIHSLIEESQNQEKNQELLEDKASLWVWF 666

RESULT 2

env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13288
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OR>
A:Cross-references: UNIPROT:O85582; UNIPROT:Q72502; UNIPROT:O90178; UNIPROT:Q78243; UNIPROT:Q78244; UNIPROT:Q78245; UNIPROT:Q78246; UNIPROT:Q78247; UNIPROT:Q78248; UNIPROT:Q78249; UNIPROT:Q78250; UNIPROT:Q78251; UNIPROT:Q78252; UNIPROT:Q78253; UNIPROT:Q78254; UNIPROT:Q78255; UNIPROT:Q78256; UNIPROT:Q78257; UNIPROT:Q78258; UNIPROT:Q78259; UNIPROT:Q78260; UNIPROT:Q78261; UNIPROT:Q78262; UNIPROT:Q78263; UNIPROT:Q78264; UNIPROT:Q78265; UNIPROT:Q78266; UNIPROT:Q78267; UNIPROT:Q78268; UNIPROT:Q78269; UNIPROT:Q78270; UNIPROT:Q78271; UNIPROT:Q78272; UNIPROT:Q78273; UNIPROT:Q78274; UNIPROT:Q78275; UNIPROT:Q78276; UNIPROT:Q78277; UNIPROT:Q78278; UNIPROT:Q78279; UNIPROT:Q78280; UNIPROT:Q78281; UNIPROT:Q78282; UNIPROT:Q78283; UNIPROT:Q78284; UNIPROT:Q78285; UNIPROT:Q78286; UNIPROT:Q78287; UNIPROT:Q78288; UNIPROT:Q78289; UNIPROT:Q78290; UNIPROT:Q78291; UNIPROT:Q78292; UNIPROT:Q78293; UNIPROT:Q78294; UNIPROT:Q78295; UNIPROT:Q78296; UNIPROT:Q78297; UNIPROT:Q78298; UNIPROT:Q78299; UNIPROT:Q78300; UNIPROT:Q78301; UNIPROT:Q78302; UNIPROT:Q78303; UNIPROT:Q78304; UNIPROT:Q78305; UNIPROT:Q78306; UNIPROT:Q78307; UNIPROT:Q78308; UNIPROT:Q78309; UNIPROT:Q78310; UNIPROT:Q78311; UNIPROT:Q78312; UNIPROT:Q78313; UNIPROT:Q78314; UNIPROT:Q78315; UNIPROT:Q78316; UNIPROT:Q78317; UNIPROT:Q78318; UNIPROT:Q78319; UNIPROT:Q78320; UNIPROT:Q78321; UNIPROT:Q78322; UNIPROT:Q78323; UNIPROT:Q78324; UNIPROT:Q78325; UNIPROT:Q78326; UNIPROT:Q78327; UNIPROT:Q78328; UNIPROT:Q78329; UNIPROT:Q78330; UNIPROT:Q78331; UNIPROT:Q78332; UNIPROT:Q78333; UNIPROT:Q78334; UNIPROT:Q78335; UNIPROT:Q78336; UNIPROT:Q78337; UNIPROT:Q78338; UNIPROT:Q78339; UNIPROT:Q78340; UNIPROT:Q78341; UNIPROT:Q78342; UNIPROT:Q78343; UNIPROT:Q78344; UNIPROT:Q78345; UNIPROT:Q78346; UNIPROT:Q78347; UNIPROT:Q78348; UNIPROT:Q78349; UNIPROT:Q78350; UNIPROT:Q78351; UNIPROT:Q78352; UNIPROT:Q78353; UNIPROT:Q78354; UNIPROT:Q78355; UNIPROT:Q78356; UNIPROT:Q78357; UNIPROT:Q78358; UNIPROT:Q78359; UNIPROT:Q78360; UNIPROT:Q78361; UNIPROT:Q78362; UNIPROT:Q78363; UNIPROT:Q78364; UNIPROT:Q78365; UNIPROT:Q78366; UNIPROT:Q78367; UNIPROT:Q78368; UNIPROT:Q78369; UNIPROT:Q78370; UNIPROT:Q78371; UNIPROT:Q78372; UNIPROT:Q78373; UNIPROT:Q78374; UNIPROT:Q78375; UNIPROT:Q78376; UNIPROT:Q78377; UNIPROT:Q78378; UNIPROT:Q78379; UNIPROT:Q78380; UNIPROT:Q78381; UNIPROT:Q78382; UNIPROT:Q78383; UNIPROT:Q78384; UNIPROT:Q78385; UNIPROT:Q78386; UNIPROT:Q78387; UNIPROT:Q78388; UNIPROT:Q78389; UNIPROT:Q78390; UNIPROT:Q78391; UNIPROT:Q78392; UNIPROT:Q78393; UNIPROT:Q78394; UNIPROT:Q78395; UNIPROT:Q78396; UNIPROT:Q78397; UNIPROT:Q78398; UNIPROT:Q78399; UNIPROT:Q78400; UNIPROT:Q78401; UNIPROT:Q78402; UNIPROT:Q78403; UNIPROT:Q78404; UNIPROT:Q78405; UNIPROT:Q78406; UNIPROT:Q78407; UNIPROT:Q78408; UNIPROT:Q78409; UNIPROT:Q78410; UNIPROT:Q78411; UNIPROT:Q78412; UNIPROT:Q78413; UNIPROT:Q78414; UNIPROT:Q78415; UNIPROT:Q78416; UNIPROT:Q78417; UNIPROT:Q78418; UNIPROT:Q78419; UNIPROT:Q78420; UNIPROT:Q78421; UNIPROT:Q78422; UNIPROT:Q78423; UNIPROT:Q78424; UNIPROT:Q78425; UNIPROT:Q78426; UNIPROT:Q78427; UNIPROT:Q78428; UNIPROT:Q78429; UNIPROT:Q78430; UNIPROT:Q78431; UNIPROT:Q78432; UNIPROT:Q78433; UNIPROT:Q78434; UNIPROT:Q78435; UNIPROT:Q78436; UNIPROT:Q78437; UNIPROT:Q78438; UNIPROT:Q78439; UNIPROT:Q78440; UNIPROT:Q78441; UNIPROT:Q78442; UNIPROT:Q78443; UNIPROT:Q78444; UNIPROT:Q78445; UNIPROT:Q78446; UNIPROT:Q78447; UNIPROT:Q78448; UNIPROT:Q78449; UNIPROT:Q78450; UNIPROT:Q78451; UNIPROT:Q78452; UNIPROT:Q78453; UNIPROT:Q78454; UNIPROT:Q78455; UNIPROT:Q78456; UNIPROT:Q78457; UNIPROT:Q78458; UNIPROT:Q78459; UNIPROT:Q78460; UNIPROT:Q78461; UNIPROT:Q78462; UNIPROT:Q78463; UNIPROT:Q78464; UNIPROT:Q78465; UNIPROT:Q78466; UNIPROT:Q78467; UNIPROT:Q78468; UNIPROT:Q78469; UNIPROT:Q78470; UNIPROT:Q78471; UNIPROT:Q78472; UNIPROT:Q78473; UNIPROT:Q78474; UNIPROT:Q78475; UNIPROT:Q78476; UNIPROT:Q78477; UNIPROT:Q78478; UNIPROT:Q78479; UNIPROT:Q78480; UNIPROT:Q78481; UNIPROT:Q78482; UNIPROT:Q78483; UNIPROT:Q78484; UNIPROT:Q78485; UNIPROT:Q78486; UNIPROT:Q78487; UNIPROT:Q78488; UNIPROT:Q78489; UNIPROT:Q78490; UNIPROT:Q78491; UNIPROT:Q78492; UNIPROT:Q78493; UNIPROT:Q78494; UNIPROT:Q78495; UNIPROT:Q78496; UNIPROT:Q78497; UNIPROT:Q78498; UNIPROT:Q78499; UNIPROT:Q78500; UNIPROT:Q78501; UNIPROT:Q78502; UNIPROT:Q78503; UNIPROT:Q78504; UNIPROT:Q78505; UNIPROT:Q78506; UNIPROT:Q78507; UNIPROT:Q78508; UNIPROT:Q78509; UNIPROT:Q78510; UNIPROT:Q78511; UNIPROT:Q78512; UNIPROT:Q78513; UNIPROT:Q78514; UNIPROT:Q78515; UNIPROT:Q78516; UNIPROT:Q78517; UNIPROT:Q78518; UNIPROT:Q78519; UNIPROT:Q78520; UNIPROT:Q78521; UNIPROT:Q78522; UNIPROT:Q78523; UNIPROT:Q78524; UNIPROT:Q78525; UNIPROT:Q78526; UNIPROT:Q78527; UNIPROT:Q78528; UNIPROT:Q78529; UNIPROT:Q78530; UNIPROT:Q78531; UNIPROT:Q78532; UNIPROT:Q78533; UNIPROT:Q78534; UNIPROT:Q78535; UNIPROT:Q78536; UNIPROT:Q78537; UNIPROT:Q78538; UNIPROT:Q78539; UNIPROT:Q78540; UNIPROT:Q78541; UNIPROT:Q78542; UNIPROT:Q78543; UNIPROT:Q78544; UNIPROT:Q78545; UNIPROT:Q78546; UNIPROT:Q78547; UNIPROT:Q78548; UNIPROT:Q78549; UNIPROT:Q78550; UNIPROT:Q78551; UNIPROT:Q78552; UNIPROT:Q78553; UNIPROT:Q78554; UNIPROT:Q78555; UNIPROT:Q78556; UNIPROT:Q78557; UNIPROT:Q78558; UNIPROT:Q78559; UNIPROT:Q78560; UNIPROT:Q78561; UNIPROT:Q78562; UNIPROT:Q78563; UNIPROT:Q78564; UNIPROT:Q78565; UNIPROT:Q78566; UNIPROT:Q78567; UNIPROT:Q78568; UNIPROT:Q78569; UNIPROT:Q78570; UNIPROT:Q78571; UNIPROT:Q78572; UNIPROT:Q78573; UNIPROT:Q78574; UNIPROT:Q78575; UNIPROT:Q78576; UNIPROT:Q78577; UNIPROT:Q78578; UNIPROT:Q78579; UNIPROT:Q78580; UNIPROT:Q78581; UNIPROT:Q78582; UNIPROT:Q78583; UNIPROT:Q78584; UNIPROT:Q78585; UNIPROT:Q78586; UNIPROT:Q78587; UNIPROT:

Query Match	100.0%;	Score 195;	DB 2;	Length 854
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```
Matches    36;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

Oy 1 YTSLIHSLIESNQOEKNEQELLELDKASLWTF 36
 |||||
Db 636 YTSLIHSLIESNQOEKNEQELLELDKASLWTF 671

RESULT 3

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VCLJTH3
env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Joseph, S.F.; Doranberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93553; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 36
DB 638 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 673

RESULT 4
VCLJTV
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:8509333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: UNIPROT:P03377; GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 100.0%; Score 195; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 36
DB 643 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 678

RESULT 5
C41621
env polypeptide P - human immunodeficiency virus type 1 (fragment)

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N:Alternate names: coat polypeptide
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: UNIPROT:Q80023; GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: cat

Query Match 95.4%; Score 186; DB 2; Length 443;
Best Local Similarity 94.4%; Pred. No. 1,3e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 36
DB 378 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 413

RESULT 6
VCLJW
env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parke, E.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; GB:K03455; GB:M84432; NID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 95.4%; Score 186; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 2,7e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 36
DB 638 YTSLSHSLIESONQOEKNEQLLELDKASLNNMF 673

RESULT 7
VCLJVL
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004

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C/Accession: A03974
R/Musing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laeky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A/Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A/Reference number: A93355; MUID:85111157; PMID:2982104
A/Accession: A03974
A/Molecule type: DNA
A/Residues: 1-856 <MSE>
A/Cross-references: UNIPROT:P03376; GB:K02083; NID:G555008; PIDN:AA59873.1; PID:G328558
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 95.4%; Score 186; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 2.7e-14;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 35
Db 638 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 678

RESULT 8
VCLISC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N/Alternate names: coat polyprotein
C/Species: human immunodeficiency virus type 1, HIV-1
A/Note: host Homo sapiens (man)
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C/Accession: B28922
R/Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A/Title: Envelope sequences of two new United States HIV-1 isolates.
A/Reference number: A28922; MUID:86219542; PMID:3369091
A/Accession: B28922
A/Molecule type: DNA
A/Residues: 1-861 <GUR>
C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein
C/Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polyprotein #status predicted <BP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 95.4%; Score 186; DB 1; Length 861;
Best Local Similarity 94.4%; Pred. No. 2.7e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 36
Db 643 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 678

RESULT 9
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 27B
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S21994; S70421
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S21994
A/Molecule type: DNA

A/Residues: 1-357 <STEL>
A/Cross-references: UNIPROT:Q78118; EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70421
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A/Cross-references: EMBL:X61355; NID:G60179
C/Superfamily: type E retrovirus env polyprotein
Query Match 93.8%; Score 183; DB 2; Length 357;
Best Local Similarity 91.7%; Pred. No. 2.4e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 36
Db 139 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 174

RESULT 10
S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
A/Variety: isolate 28
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S21998; S70425
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A/Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A/Reference number: S21990
A/Accession: S21998
A/Molecule type: DNA
A/Residues: 1-358 <STEL>
A/Cross-references: UNIPROT:Q78120; EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70425
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-222, 'X', 224-358 <STE2>
A/Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
C/Superfamily: type E retrovirus env polyprotein
Query Match 93.8%; Score 183; DB 2; Length 358;
Best Local Similarity 91.7%; Pred. No. 2.4e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 36
Db 140 YTSLSHLSIESNQOEKNEQELLELDKASLWMP 175

RESULT 11
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S70422; S21996
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A/Reference number: S70417; MUID:92144209; PMID:11736940
A/Accession: S70422
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-357 <STE2>
A/Cross-references: UNIPROT:Q78119; EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G10671;
A/Experimental source: patient 27L

A/Note: submitted to the EMBL Data Library, July 1991
C/Superfamily: type E retrovirus env polyprotein

Query Match 93.3%; Score 182; DB 2; Length 357;
Best Local Similarity 91.7%; Pred. No. 1.1e-13;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 36
DB 139 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 174

RESULT 12

T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JHFL)

C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09448
R/Pang: S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, R.; submitted to the EMBL Data Library, July 1996

A/Reference number: Z16673
A/Accession: T09448
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-847 <PAN>

A/Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:G1465777; PID:G1465781

C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein

Query Match 91.8%; Score 179; DB 2; Length 847;
Best Local Similarity 91.7%; Pred. No. 1.8e-13;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 36
DB 629 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 664

RESULT 13

S13289
env protein - human immunodeficiency virus type 1

C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 16-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S13289
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A/Reference number: S13288; MUID:91043044; PMID:2172833

A/Accession: S13289

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-847 <OBR>

A/Cross-references: UNIPROT:Q75760

C/Superfamily: type E retrovirus env polyprotein

Query Match 91.8%; Score 179; DB 2; Length 847;
Best Local Similarity 91.7%; Pred. No. 1.8e-13;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 14

A41621
env polyprotein M - human immunodeficiency virus type 1 (fragment)

N/Alternate names: coat polyprotein

N/Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A41621
R/Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A/Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A/Reference number: A41621; MUID:92107924; PMID:1763038

A/Accession: A41621

A/Molecule type: DNA

A/Residues: 1-445 <BUR>

A/Cross-references: UNIPROT:Q80021; GB:M77228; NID:G328627; PIDN:AAB03790.1; PID:G555013

A/Note: this virus was isolated from the mother

C/Genetics:
A/Gene: env
C/Superfamily: type E retrovirus env polyprotein

C/Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote

F/1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F/254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F/426-445/Domain: transmembrane #status predicted <TMN>

F/23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 91.3%; Score 178; DB 2; Length 445;
Best Local Similarity 88.9%; Pred. No. 1.2e-13;
Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 36
DB 380 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 415

RESULT 15

S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)

C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S70417
R/Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A/Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A/Reference number: S70417; MUID:92144209; PMID:1736940

A/Accession: S70417

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-358 <STE>

A/Cross-references: UNIPROT:Q78140; EMBL:X61351; NID:G60184; PIDN:CAA43614.1; PID:G60185

C/Superfamily: type E retrovirus env polyprotein

Query Match 90.8%; Score 177; DB 2; Length 358;
Best Local Similarity 88.9%; Pred. No. 1.2e-13;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 36
DB 140 YTSLSHSLIESONQOEKNEQELLELDKMASLWMP 175

Search completed: September 20, 2005, 19:48:29
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2005, 19:24:39 ; Search time 173 Seconds
(without alignments)
106.560 Million cell updates/sec

Title: US-09-809-060A-1
Perfect score: 195
Sequence: 1 YTSLSHSLIESQNOCKNEQELLEDKMSLWNMF 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	645	2 Q993A6	Q993A6 human immun
2	195	100.0	747	2 Q70607	Q70607 human immun
3	195	100.0	748	2 Q70606	Q70606 human immun
4	195	100.0	752	2 Q70604	Q70604 human immun
5	195	100.0	752	2 Q70605	Q70605 human immun
6	195	100.0	752	2 Q70608	Q70608 human immun
7	195	100.0	851	1 ENV_HV1B8	P04582 human immun
8	195	100.0	851	2 Q78243	Q78243 human immun
9	195	100.0	852	2 Q6TAP8	Q6TAP8 human immun
10	195	100.0	852	2 Q6TAP9	Q6TAP9 human immun
11	195	100.0	852	2 Q6TAQ1	Q6TAQ1 human immun
12	195	100.0	852	2 Q6TAQ2	Q6TAQ2 human immun
13	195	100.0	852	2 Q6TAQ3	Q6TAQ3 human immun
14	195	100.0	852	2 Q6TAQ4	Q6TAQ4 human immun
15	195	100.0	852	2 Q6TAP5	Q6TAP5 human immun
16	195	100.0	852	2 Q6TAP7	Q6TAP7 human immun
17	195	100.0	854	2 Q6BC06	Q6BC06 human immun
18	195	100.0	854	2 Q6TAN3	Q6TAN3 human immun
19	195	100.0	854	2 Q6TAN4	Q6TAN4 human immun
20	195	100.0	854	2 Q6TAN5	Q6TAN5 human immun
21	195	100.0	854	2 Q6TAN6	Q6TAN6 human immun
22	195	100.0	854	2 Q6TAN7	Q6TAN7 human immun
23	195	100.0	854	2 Q6TAN8	Q6TAN8 human immun
24	195	100.0	854	2 Q72502	Q72502 human immun
25	195	100.0	854	2 Q85582	Q85582 human immun
26	195	100.0	856	1 ENV_HV1B1	P03375 human immun
27	195	100.0	856	1 ENV_HV1B2	P04578 human immun
28	195	100.0	856	1 ENV_HV1B3	P04626 human immun
29	195	100.0	856	1 ENV_HV1B4	Q70626 human immun
30	195	100.0	856	1 Q92877	Q92877 simj en-huma
31	195	100.0	856	2 Q74090	Q74090 human immun

32	195	100.0	856	2 Q74599	Q74599 human immun
33	195	100.0	861	1 ENV_HV1B8	P03377 human immun
34	192	98.5	853	1 ENV_HV1M6	P19551 human immun
35	191	97.9	854	2 Q90178	Q90178 human immun
36	191	97.9	854	2 Q78705	Q78705 human immun
37	190	97.4	856	2 Q90SM7	Q90SM7 human immun
38	189	96.9	616	2 Q993B0	Q993B0 human immun
39	189	96.9	618	2 Q993B2	Q993B2 human immun
40	189	96.9	757	2 Q9Q722	Q9Q722 human immun
41	189	96.9	847	2 Q72820	Q72820 human immun
42	189	96.9	848	2 Q69990	Q69990 human immun
43	187	95.9	144	2 Q7ZCB7	Q7ZCB7 human immun
44	187	95.9	809	2 Q6QL15	Q6QL15 human immun
45	187	95.9	838	2 Q03806	Q03806 human immun

ALIGNMENTS

```

RESULT 1
Q993A6 PRELIMINARY; PRT; 645 AA.
ID Q993A6;
AC Q993A6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192672; PubMed=11287644; DOI=10.1073/pnas.071063898;
RA Surman S., Lockey T.D., Stobod K.S., Jones B., Riberty J.M.,
RA White S.W., Doherty P.C., Hurwitz J.L.;
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of
RT HIV envelope glycoprotein suggests structural influences on antigen
RT processing";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).
DR EMBL; AF321563; AKI18810.1; -.
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
SQ
SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;
QY 1 YTSLSHSLIESQNOCKNEQELLEDKMSLWNMF 36
Db 607 YTSLSHSLIESQNOCKNEQELLEDKMSLWNMF 642

Query Match 100.0%; Score 195; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
Q70607 PRELIMINARY; PRT; 747 AA.
ID Q70607;
AC Q70607;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;

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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA7666.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON TER
SQ SEQUENCE 747 AA; 84250 MW; 732B836A52245F14 CRC64;

Query Match 100.0%; Score 195; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 36
DB 633 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 668

RESULT 3
OY 070606 PRELIMINARY; PRT; 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT -01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA7666.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON TER
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 195; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 36
DB 634 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 669

RESULT 4
OY 070604 PRELIMINARY; PRT; 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA7666.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON TER
SQ SEQUENCE 752 AA; 84894 MW; 8B30AB894013B45A CRC64;

Query Match 100.0%; Score 195; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 36
DB 638 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 673

RESULT 5
OY 070605 PRELIMINARY; PRT; 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).

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DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON TER
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 195; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 36
DB 634 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 669

RESULT 4
OY 070604 PRELIMINARY; PRT; 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA7666.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00517; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON TER
SQ SEQUENCE 752 AA; 84894 MW; 8B30AB894013B45A CRC64;

Query Match 100.0%; Score 195; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 36
DB 638 YTSLIHSLSIESONQOEKNEDELLELDKWSLIMNWF 673

RESULT 5
OY 070605 PRELIMINARY; PRT; 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).

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GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; Pubmed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIB).";
RU AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Mulder K.E.;
RU Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AAA76667.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
  Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 195; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLELDKMSLWNMF 36
Db 638 YTSLSHLSIESQNOQEKNEQELLELDKMSLWNMF 673

RESULT 6
ID 070608 PRELIMINARY; PRT; 752 AA.
AC 070608;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; Pubmed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIB).";
RU AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Mulder K.E.;
RU Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12035; AAA76670.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
  Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84779 MW; 708672A2D0C0E8F8 CRC64;

Query Match 100.0%; Score 195; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLELDKMSLWNMF 36
Db 638 YTSLSHLSIESQNOQEKNEQELLELDKMSLWNMF 673

RESULT 7
ID ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN Name=ENV;
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; Pubmed=2578615;
RA Ratner L., Haseltine W.A., Patarca R., Lyak K.J., Starcich B.R.,
  Joseph S.F., Doran E.R., Rataleki J.A., Whitehorn E.A.,
  Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
  Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
  Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RU Nature 313:277-284(1985).
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CC -----
DR EMBL; K02011; AAA44661.1; -.
DR PDB; 1D0H; X-ray; P=311-320.
DR PDB; 1H8G; X-ray; C/F=192-200.
DR PDB; 1Q03; X-ray; P=311-320.
DR PDB; 1S2T; X-ray; @=541-650.
DR HIV; K02011; ENV5B8.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KM 3D-structure; AIDS; Coat protein; Glycoprotein; Polypeptide; Signal;
  Transmembrane.
FT SIGNAL 1 30
FT CHAIN 31 506 Exterior membrane glycoprotein.
FT CHAIN 507 851 Transmembrane glycoprotein.
FT DISULFID 54 74 By similarity.
FT DISULFID 119 205 By similarity.
FT DISULFID 126 196 By similarity.
FT DISULFID 131 157 By similarity.
FT DISULFID 216 247 By similarity.
FT DISULFID 228 239 By similarity.
FT DISULFID 296 331 By similarity.
FT DISULFID 378 440 By similarity.

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FT DISULFID 385 413 By similarity.
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 156 156 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 197 197 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 230 230 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 234 234 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 262 262 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 276 276 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 332 332 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 339 339 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 356 356 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 366 366 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 392 392 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 401 401 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 443 443 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 458 458 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 606 606 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 611 611 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 620 620 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 632 632 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 669 669 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 745 745 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 811 811 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 100.0%; Score 195; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSLSHLSIESQNOQEKNOEQLLELDKWSLMMWF 36
DB 633 YTSLSHLSIESQNOQEKNOEQLLELDKWSLMMWF 668

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RESULT 8
ID 078243 PRELIMINARY; PRT; 851 AA.
AC 078243;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Env polypeptide.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federico M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
RT producer clones from HUT-78 infected with a patient HIV isolate.";
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Tilti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Boretti A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
RT productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Carlini F., Federico M., Equestre M., Ricci S., Ratti G., Zibai Q.,
RA Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer

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```

RT chronically infected HUT-78 cellular clone.";
RL J. Viral Dis. 1:40-55(1992).
DR EMBL; J11530; CAA77628.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR PIR; S33985; S33985.
DR HSRP; P04576; IATK.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 851 AA; 96629 MW; 1A3767B987E98027 CRC64;

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Query Match 100.0%; Score 195; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSLSHLSIESQNOQEKNOEQLLELDKWSLMMWF 36
DB 633 YTSLSHLSIESQNOQEKNOEQLLELDKWSLMMWF 668

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RESULT 9
ID 067AP8 PRELIMINARY; PRT; 852 AA.
AC 067AP8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor
RT Switching.";
RL J. Virol. 78:7565-7574(2004).
DR EMBL; AY426109; AAR05833.1; -.
DR EMBL; AY426107; AAR05831.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96903 MW; 3F5B7D44DBE6FBFC CRC64;

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Query Match 100.0%; Score 195; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 YTSLSHLSIESQNOQEKNOEQLLELDKWSLMMWF 36
DB 634 YTSLSHLSIESQNOQEKNOEQLLELDKWSLMMWF 669

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RESULT 10
ID 067AP9 PRELIMINARY; PRT; 852 AA.
AC 067AP9;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env,
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426108; AAR05832.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 852 AA; 96971 MW; 1E186AD2DE50F57E CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLEDKXASLMMWF 36
DB 634 YTSLSHLSLEESQNOQEKNEQELLEDKXASLMMWF 669

RESULT 11
O6TA01 PRELIMINARY; PRT; 852 AA.
AC O6TA01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env,
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426108; AAR05830.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 852 AA; 97001 MW; 8DF59CADBD8AC145E CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YTSLSHLSLEESQNOQEKNEQELLEDKXASLMMWF 36
DB 634 YTSLSHLSLEESQNOQEKNEQELLEDKXASLMMWF 669

RESULT 12
O6TA02 PRELIMINARY; PRT; 852 AA.
AC O6TA02;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env,
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426105; AAR05829.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 852 AA; 96862 MW; E9D1E7BE8CD93B12 CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLEDKXASLMMWF 36
DB 634 YTSLSHLSLEESQNOQEKNEQELLEDKXASLMMWF 669

RESULT 13
O6TA03 PRELIMINARY; PRT; 852 AA.
AC O6TA03;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env,
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426104; AAR05828.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
```

DR Pfam: PF00517; GP1, 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KM Transmembrane.
 SQ SEQUENCE 852 AA; 96835 MW; 92EE2A98CD93B16 CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHSLIEESQNOEKNEQELLELDKMASLWNMF 36
 |||||
 DB 634 YTSLIHSLIEESQNOEKNEQELLELDKMASLWNMF 669

RESULT 14

O6TAQ4 PRELIMINARY; PRT; 852 AA.

AC O6TAQ4: 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OK NCBI_TaxID=11676;
 RN (1)

RP SEQUENCE FROM N.A.
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;

RA Pastore C., Ramos A., Mosier D.E.;
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor

Switching.";
 RT J. Virol. 78:7565-7574(2004) .
 DR EMBL: AY426103; AAR05826.1; -.

DR HSP: P04578; IAIK.
 DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.

DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000328; Env GP41.

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120. 1.

DR Pfam: PF00517; GP41. 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KM Transmembrane.

SQ SEQUENCE 852 AA; 96860 MW; 62B20D94FC1FF7A CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHSLIEESQNOEKNEQELLELDKMASLWNMF 36
 |||||
 DB 634 YTSLIHSLIEESQNOEKNEQELLELDKMASLWNMF 669

RESULT 15

O6TAQ5 PRELIMINARY; PRT; 852 AA.

AC O6TAQ5: 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OK NCBI_TaxID=11676;
 RN (1)

RP SEQUENCE FROM N.A.
 RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;

RA Pastore C., Ramos A., Mosier D.E.;
 RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor

Switching.";
 RT J. Virol. 78:7565-7574(2004) .
 DR EMBL: AY426102; AAR05826.1; -.

DR HSP: P04578; IAIK.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.

DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.

DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120. 1.
 DR Pfam: PF00517; GP41. 1.

KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KM Transmembrane.

SQ SEQUENCE 852 AA; 96860 MW; 62B20D94FC1FF7A CRC64;

Query Match 100.0%; Score 195; DB 2; Length 852;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHSLIEESQNOEKNEQELLELDKMASLWNMF 36
 |||||
 DB 634 YTSLIHSLIEESQNOEKNEQELLELDKMASLWNMF 669

Search completed: September 20, 2005, 19:47:44
 Job time : 175 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2005, 19:38:10 : Search time 42 Seconds
(without alignments)
63.985 Million cell updates/sec

Title: US-09-809-060A-1
Perfect score: 195
Sequence: 1 YTSLSHSLIESQNOEKNEQELLELDKASLWNMF 36

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pdp: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pdp: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pdp: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pdp: *
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pdp: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pdp: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	36	1 US-08-073-028-1	Sequence 1, Appl1
2	195	100.0	36	3 US-08-486-099-1	Sequence 1, Appl1
3	195	100.0	36	3 US-09-071-877-1	Sequence 1, Appl1
4	195	100.0	36	3 US-08-360-107A-1	Sequence 1, Appl1
5	195	100.0	36	3 US-08-484-223B-1	Sequence 1, Appl1
6	195	100.0	36	3 US-08-919-597-1	Sequence 1, Appl1
7	195	100.0	36	3 US-08-475-668A-1	Sequence 1, Appl1
8	195	100.0	36	3 US-08-485-551A-1	Sequence 1, Appl1
9	195	100.0	36	3 US-08-471-913A-1	Sequence 1, Appl1
10	195	100.0	36	3 US-08-554-616-1	Sequence 1, Appl1
11	195	100.0	36	3 US-08-485-264A-1	Sequence 1, Appl1
12	195	100.0	36	3 US-09-082-279B-15	Sequence 15, Appl1
13	195	100.0	36	3 US-09-082-279B-497	Sequence 497, Appl1
14	195	100.0	36	3 US-09-082-279B-498	Sequence 498, Appl1
15	195	100.0	36	3 US-09-082-279B-603	Sequence 603, Appl1
16	195	100.0	36	3 US-09-082-279B-630	Sequence 630, Appl1
17	195	100.0	36	3 US-09-082-279B-631	Sequence 631, Appl1
18	195	100.0	36	3 US-09-082-279B-705	Sequence 705, Appl1
19	195	100.0	36	3 US-09-082-279B-834	Sequence 834, Appl1
20	195	100.0	36	3 US-09-082-279B-1076	Sequence 1076, Appl1
21	195	100.0	36	3 US-09-082-279B-1121	Sequence 1121, Appl1
22	195	100.0	36	3 US-09-082-279B-1161	Sequence 1161, Appl1
23	195	100.0	36	3 US-08-965-056-108	Sequence 108, Appl1
24	195	100.0	36	3 US-08-965-056-108	Sequence 108, Appl1
25	195	100.0	36	3 US-09-045-920-1	Sequence 1, Appl1
26	195	100.0	36	3 US-08-474-349A-1	Sequence 1, Appl1
27	195	100.0	36	3 US-08-474-349A-399	Sequence 399, Appl1

28	195	100.0	36	3 US-08-474-349A-413	Sequence 413, Appl1
29	195	100.0	36	3 US-09-315-304B-15	Sequence 15, Appl1
30	195	100.0	36	3 US-09-315-304B-497	Sequence 497, Appl1
31	195	100.0	36	3 US-09-315-304B-498	Sequence 498, Appl1
32	195	100.0	36	3 US-09-315-304B-603	Sequence 603, Appl1
33	195	100.0	36	3 US-09-315-304B-630	Sequence 630, Appl1
34	195	100.0	36	3 US-09-315-304B-631	Sequence 631, Appl1
35	195	100.0	36	3 US-09-315-304B-705	Sequence 705, Appl1
36	195	100.0	36	3 US-09-315-304B-834	Sequence 834, Appl1
37	195	100.0	36	3 US-09-315-304B-1076	Sequence 1076, Appl1
38	195	100.0	36	3 US-09-315-304B-1121	Sequence 1121, Appl1
39	195	100.0	36	3 US-09-315-304B-1161	Sequence 1161, Appl1
40	195	100.0	36	3 US-09-315-304B-1469	Sequence 1469, Appl1
41	195	100.0	36	3 US-09-315-304B-1470	Sequence 1470, Appl1
42	195	100.0	36	3 US-09-315-304B-1486	Sequence 1486, Appl1
43	195	100.0	36	4 US-08-255-208A-1	Sequence 1, Appl1
44	195	100.0	36	4 US-08-573-952-1	Sequence 1, Appl1
45	195	100.0	36	4 US-08-470-896-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-073-028-1
; Sequence 1, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Biolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-073-028-1
Query Match 100.0%; Score 195; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIESQNOEKNEQELLELDKASLWNMF 36
|||||

Db 1 YTSLSLSIESQNOQEKNEQLLELDKMASLWNMF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSIESQNOQEKNEQLLELDKMASLWNMF 36

Db 1 YTSLSLSIESQNOQEKNEQLLELDKMASLWNMF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichy, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSIESQNOQEKNEQLLELDKMASLWNMF 36

Db 1 YTSLSLSIESQNOQEKNEQLLELDKMASLWNMF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSIESQNOQEKNEQLLELDKMASLWNMF 36

Db 1 YTSLSHSLIESQNOQEKNEQELLEDKWSLWNMF 36

RESULT 5
US-08-484-223B-1
Sequence 1, Application US/08484223B

Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-08-919-597-1
Sequence 1, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLSHSLIESQNOQEKNEQELLEDKWSLWNMF 36

RESULT 7
US-08-475-668A-1
Sequence 1, Application US/08475668A

Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36
1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36

Db 1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36

RESULT 8
US-08-485-551A-1
Sequence 1, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36
1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36

Db 1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36

RESULT 9
US-08-471-913A-1
Sequence 1, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36
1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36

Db 1 YTSLSLSIESQNOQEKNEQELLELDKWSLMMWF 36

RESULT 10
US-08-554-616-1
Sequence 1, Application US/08554616
Patent No. 6133418
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,028
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSIESNQOEKNEQELLELDKWSLWNMF 36
Db 1 YTSLSLSIESNQOEKNEQELLELDKWSLWNMF 36

RESULT 11
US-08-485-264A-1
Sequence 1, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-1

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSIESNQOEKNEQELLELDKWSLWNMF 36
Db 1 YTSLSLSIESNQOEKNEQELLELDKWSLWNMF 36

RESULT 12
US-09-082-279B-15
Sequence 15, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Murtuka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-15

Query Match 100.0%; Score 195; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSIESNQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

RESULT 13

US-09-082-279B-497

; Sequence 497, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 497

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

Db 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

RESULT 14

US-09-082-279B-498

; Sequence 498, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 498

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

Db 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

RESULT 15

US-09-082-279B-603

; Sequence 603, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 603

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

Db 1 YTSLSHSLIESONQOEKNEQELLEDKVASLWNMF 36

Search completed: September 20, 2005, 19:49:18
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: September 20, 2005, 19:42:06 ; Search time 168 Seconds
(without alignments)
86.770 Million cell updates/sec

Title: US-09-809-060A-1
Perfect score: 195
Sequence: 1 YTSLSHSLIESQNOEKNEQELLEDKMSLWNMF 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep:*
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21: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
22: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	195	100.0	36 9 US-09-809-060-85	Sequence 85, Appli
3	195	100.0	36 9 US-09-796-202-10	Sequence 10, Appli
4	195	100.0	36 9 US-09-960-717-2	Sequence 2, Appli
5	195	100.0	36 9 US-09-779-451-5	Sequence 5, Appli
6	195	100.0	36 9 US-09-834-628-1	Sequence 1, Appli
7	195	100.0	36 9 US-09-828-615-1	Sequence 1, Appli
8	195	100.0	36 9 US-09-854-816-1	Sequence 1, Appli
9	195	100.0	36 9 US-09-854-816-108	Sequence 108, Appli
10	195	100.0	36 9 US-09-874-475-16	Sequence 16, Appli
11	195	100.0	36 10 US-09-493-346-1	Sequence 1, Appli

12	195	100.0	36 14 US-10-116-797-1	Sequence 1, Appli
13	195	100.0	36 14 US-10-252-136-1	Sequence 1, Appli
14	195	100.0	36 14 US-10-158-742A-8	Sequence 8, Appli
15	195	100.0	36 14 US-10-323-314-10	Sequence 10, Appli
16	195	100.0	36 14 US-10-278-364A-7	Sequence 7, Appli
17	195	100.0	36 14 US-10-351-641-15	Sequence 15, Appli
18	195	100.0	36 14 US-10-351-641-497	Sequence 497, App
19	195	100.0	36 14 US-10-351-641-498	Sequence 498, App
20	195	100.0	36 14 US-10-351-641-603	Sequence 603, App
21	195	100.0	36 14 US-10-351-641-630	Sequence 630, App
22	195	100.0	36 14 US-10-351-641-631	Sequence 631, App
23	195	100.0	36 14 US-10-351-641-705	Sequence 705, App
24	195	100.0	36 14 US-10-351-641-834	Sequence 834, App
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33	195	100.0	36 15 US-10-005-305-197	Sequence 197, App
34	195	100.0	36 15 US-10-378-094-17	Sequence 17, Appli
35	195	100.0	36 15 US-10-420-194-1233	Sequence 1233, App
36	195	100.0	36 15 US-10-231-494-14	Sequence 14, Appli
37	195	100.0	36 15 US-10-267-682-1	Sequence 1, Appli
38	195	100.0	36 15 US-10-623-873-1	Sequence 1, Appli
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41	195	100.0	36 15 US-10-663-589-4	Sequence 4, Appli
42	195	100.0	36 15 US-10-469-199-9	Sequence 9, Appli
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44	195	100.0	36 16 US-10-164-290A-16	Sequence 16, Appli
45	195	100.0	36 16 US-10-671-282-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-809-060-1
; Sequence 1, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-1

Query Match 100.0%; Score 195; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTSLSHSLIESQNOEKNEQELLEDKMSLWNMF 36

RESULT 2
US-09-809-060-85

; Sequence 85, Application US/09809060
; Publication No. US2002010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-85

Query Match 100.0%; Score 195; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTSLSHSLIESQNOQEKNEQELLELDKVASLWNMF 36

RESULT 3
US-09-796-202-10
; Sequence 10, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olsson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: T-20
US-09-796-202-10

Query Match 100.0%; Score 195; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTSLSHSLIESQNOQEKNEQELLELDKVASLWNMF 36

RESULT 4
US-09-960-717-2
; Sequence 2, Application US/09960717
; Publication No. US20020086283A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: PATEL, DHAVALKUMAR D.
; APPLICANT: ALAM, MUNIR
; APPLICANT: LIAO, HUA-XIN
; TITLE OF INVENTION: IMMUNOGEN
; FILE REFERENCE: 1579-599

; CURRENT APPLICATION NUMBER: US/09/960,717
; CURRENT FILING DATE: 2001-09-16
; PRIOR APPLICATION NUMBER: 60/234,327
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/285,173
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/323,697
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/323,702
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human Immunodeficiency Virus
US-09-960-717-2

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Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTSLSHSLIESQNOQEKNEQELLELDKVASLWNMF 36

RESULT 5
US-09-779-451-5
; Sequence 5, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-5

Query Match 100.0%; Score 195; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTSLSHSLIESQNOQEKNEQELLELDKVASLWNMF 36

RESULT 6
US-09-834-628-1
; Sequence 1, Application US/09834628
; Patent No. US20020119922A1
; GENERAL INFORMATION:
; APPLICANT: YU, YEON GYU
; APPLICANT: KIM, KEY-SUN
; APPLICANT: JIN, BONG-SUK
; TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION
; FILE REFERENCE: 05823.0198-00000
; CURRENT APPLICATION NUMBER: US/09/834,628
; CURRENT FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: KR 00-65664
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 1
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
OTHER INFORMATION: Dp178
US-09-834-628-1

Query Match
Best Local Similarity 100.0%; Score 195; DB 9; Length 36;
Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTSLSLHSLIESQNOQEKNEQELLELDKMASLWVNF 36

RESULT 7
US-09-828-615-1
Sequence 1, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828,615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-1

Query Match
Best Local Similarity 100.0%; Score 195; DB 9; Length 36;
Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YTSLSLHSLIESQNOQEKNEQELLELDKMASLWVNF 36

RESULT 8
US-09-854-816-1
Sequence 1, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Dp178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-854-816-1

Query Match
Best Local Similarity 100.0%; Score 195; DB 9; Length 36;
Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLHSLIESQNOQEKNEQELLELDKMASLWVNF 36
DB 1 YTSLSLHSLIESQNOQEKNEQELLELDKMASLWVNF 36

RESULT 9
US-09-854-816-108
Sequence 108, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-854-816-108
SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Query Match 100.0%; Score 195; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
US-09-874-475-16
Sequence 16, Application US/09874475
Publication No. US20020182592A1
GENERAL INFORMATION:
APPLICANT: Petropoulos, Christos J.
APPLICANT: Parkin, Neil T.
APPLICANT: Whitcomb, Jeanette
APPLICANT: Huang, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECEPTOR
TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS
FILE REFERENCE: 2793/65166
CURRENT APPLICATION NUMBER: US/09/874,475
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 36
TYPE: PRT
ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match 100.0%; Score 195; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36

RESULT 11
US-09-493-346-1
Sequence 1, Application US/09493346
Publication No. US20030082185A1
GENERAL INFORMATION:
APPLICANT: Olson, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
TITLE OF INVENTION: Infection
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/09/493,346
CURRENT FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide
US-09-493-346-1

Query Match 100.0%; Score 195; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36
1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36

RESULT 12
US-10-116-797-1
Sequence 1, Application US/10116797
Publication No. US2003004411A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-1

Query Match 100.0%; Score 195; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36
1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36

RESULT 13
US-10-252-136-1
Sequence 1, Application US/10252136
Publication No. US2003010398A1
GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/10/252,136
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/08/973,952
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 36
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-252-136-1

Query Match 100.0%; Score 195; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36
1 YTSLSLIEESQNOEKNEQELLEDKWSLMMNF 36

RESULT 14
US-10-158-742A-8
Sequence 8, Application US/10158742A
Publication No. US20030104581A1

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; GENERAL INFORMATION:
; APPLICANT: Hoeess, Eva
; APPLICANT: Meier, Thomas
; APPLICANT: Pestlin, Gabriele
; APPLICANT: Popp, Friedrich
; APPLICANT: Reichert, Klaus
; APPLICANT: Schmuck, Rainer
; APPLICANT: Schneider, Bernd
; APPLICANT: Seidel, Christoph
; APPLICANT: Tischer, Wilhelm
; TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM
; FILE REFERENCE: 20904
; CURRENT APPLICATION NUMBER: US/10/158,742A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: EP 0114497.9
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide T680
US-10-158-742A-8

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Query Match      100.0%; Score 195; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 YTSLSHLSIESQNOEKNEQELLEDKMSLWNMF 36

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RESULT 15
US-10-323-314-10
; Sequence 10. Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Draglic, Tatjana
; APPLICANT: Olsson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: T-20
US-10-323-314-10

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Query Match      100.0%; Score 195; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
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- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Query Match	Length	ID	Description
1	36	100.0	36	2	AAR64364 DP-178 de
2	36	100.0	36	2	AAR98398 DP178 cor
3	36	100.0	36	2	AAW17011 HIV-1 der
4	36	100.0	36	2	AAy22912 SEQ ID NO
5	36	100.0	36	2	AAy22805 SEQ ID NO
6	36	100.0	36	2	AAy31974 HIV-1 LAI
7	36	100.0	36	2	AAy31955 Synthetic
8	36	100.0	36	3	AAy89999 Core poly
9	36	100.0	36	3	AAy88665 Core poly
10	36	100.0	36	3	AAy89777 Core poly
11	36	100.0	36	3	AAy89982 Core poly
12	36	100.0	36	3	AAy89424 Core poly
13	36	100.0	36	3	AAy89692 Core poly
14	36	100.0	36	3	AAy89242 Core poly
15	36	100.0	36	3	AAy89983 Core poly
16	36	100.0	36	3	AAy88729 Core poly
17	36	100.0	36	3	AAy89135 Core poly
18	36	100.0	36	3	AAy89136 Core poly
19	36	100.0	36	3	AAy89735 Core poly
20	36	100.0	36	3	AAy14533 HIV-1 iso
21	36	100.0	36	3	AAy52818 T20/DP178
22	36	100.0	36	3	AAy52655 T20/DP178
23	36	100.0	36	3	AAy52688 T20/DP178
24	36	100.0	36	4	AAy63861 Amino aci
25	36	100.0	36	4	AAy54784 HIV anti

26	36	100.0	36	4	AAy54902 Anti-HIV
27	36	100.0	36	4	AAy54935 Anti-HIV
28	36	100.0	36	4	AAy92243 Virus rel
29	36	100.0	36	4	AAy92352 Virus rel
30	36	100.0	36	4	AAy77083 Core poly
31	36	100.0	36	4	AAy78136 Core poly
32	36	100.0	36	4	AAy78400 Core poly
33	36	100.0	36	4	AAy77595 Core poly
34	36	100.0	36	4	AAy77020 Core poly
35	36	100.0	36	4	AAy77084 Core poly
36	36	100.0	36	4	AAy77622 Core poly
37	36	100.0	36	4	AAy77623 Core poly
38	36	100.0	36	4	AAy78178 Core poly
39	36	100.0	36	4	AAy77490 Core poly
40	36	100.0	36	4	AAy78384 Core poly
41	36	100.0	36	4	AAy77491 Core poly
42	36	100.0	36	4	AAy77621 Core poly
43	36	100.0	36	4	AAy78383 Core poly
44	36	100.0	36	4	AAy77825 Core poly
45	36	100.0	36	4	AAy78093 Core poly

ALIGNMENTS

RESULT 1					
AAy64364	AAy64364 standard; peptide; 36 AA.				
XX					
AC	AAy64364;				
XX					
DT	25-MAR-2003 (revised)				
DT	24-AUG-1995 (first entry)				
XX					
DE	DP-178 derived from HIV-1 isolate LAI has antiviral activity.				
XX					
KM	antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;				
KM	human immunodeficiency virus; transmembrane protein; gp41; alpha helix;				
KW	leucine zipper; DP-185.				
XX					
OS	Synthetic.				
XX					
FM	Key				
FT	Modified-site				
FT	1 /note="optionally has an amino, acetyl, 9-fluorenylmethoxy-carbonyl, hydrophobic or macromolecular carrier gp. attached"				
FT	Modified-site				
XX	38 /note="optionally has a carboxyl, amido, hydrophobic or macromolecular carrier gp. attached"				
PN	W09428920-A1.				
XX					
PD	22-DEC-1994.				
XX					
PF	07-JUN-1994; 94MO-US005739.				
XX					
PR	07-JUN-1993; 93US-00073028.				
XX					
PA	(UYDU-) UNIV DUKE.				
XX					
PI	Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM; Petteway SR;				
XX	WPI; 1995-036105/05.				
DR					
XX					
PT	Computer search generated synthetic peptides - are inhibitors of HIV transmission.				
PS	Claim 11; Page 132; 182pp; English.				
XX					
CC	AAy64364 is designated DP-178, and corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative				

CC alpha helix at the C-terminal end of the gp41 ectodomain, and complexes
 CC with DP-107 (corresponds to amino acids 558-595) which contains a leucine
 CC zipper motif. The peptides complex via non-covalent protein-protein
 CC interactions, and possess anti-viral activity. Homologues of these
 CC peptides were identified by a computer assisted peptide sequence search.
 CC The peptides inhibit transmission to uninfected cells, and can also be
 CC used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR
 CC -2003 to correct PN field.)
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLSLHSLIESQNOQEKNEQELLEDKVASLWNMF 36
 DB 1 YTSLSLHSLIESQNOQEKNEQELLEDKVASLWNMF 36
 RESULT 2
 AAR98398
 ID AAR98398 standard; peptide; 36 AA.
 XX
 AC AAR98398;
 XX
 DT 16-OCT-2003 (revised)
 DT 17-FEB-1997 (first entry)
 XX
 DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.
 XX
 KM Antifusogenic activity; antiviral capability; coiled-coil peptide;
 KM ALUMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;
 KM influenza virus; hepatitis B virus.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN MO9619495-A1.
 XX
 PD 27-JUN-1996.
 XX
 PF 20-DEC-1995; 95MO-US016733.
 XX
 PR 20-DEC-1994; 94US-00360107.
 PR 06-JUN-1995; 95US-00470896.
 XX
 PA (UYDU-) UNIV DUKE.
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Bolognesi DP, Matthews TU, Wild CT, Barney S, Lambert DM;
 PI Pellew SR, Langlois AU;
 XX
 DR WPI; 1996-309517/31.
 XX
 PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an
 PT isolated peptide recognised by an ALUMOTIS, 107x178x4 or PLZIP sequence
 PT search motif.
 XX
 PS Disclosure; Fig 1; 471pp; English.
 XX
 CC The sequences given in AAR98398-408 represent peptides which exhibit
 CC antifusogenic activity, antiviral capability and/or the ability to
 CC modulate intracellular processes involving coiled-coil peptide
 CC structures. These peptides are recognised by the ALUMOTIS, 107x178x4 and
 CC PLZIP search motifs. These peptides may be used to inhibit the
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLHSLIESQNOQEKNEQELLEDKVASLWNMF 36
 DB 1 YTSLSLHSLIESQNOQEKNEQELLEDKVASLWNMF 36
 RESULT 3
 AAM17011
 ID AAM17011 standard; peptide; 36 AA.
 XX
 AC AAM17011;
 XX
 DT 17-OCT-2003 (revised)
 DT 30-JUN-1997 (first entry)
 XX
 DE HIV-1 derived peptide useful for treatment of HIV infection.
 XX
 KM HIV; STV; human; simian immunodeficiency virus; glycoprotein 41;
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;
 KM replication; transmission.
 XX
 OS Human immunodeficiency virus 1; LAI isolate.
 XX
 PN MO9640191-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WC-US009499.
 XX
 PR 07-JUN-1995; 95US-00481957.
 XX
 PA (TRIM-) TRIMERIS INC.
 PA Johnson RM, Lambert DM;
 PI
 XX
 DR WPI; 1997-099886/09.
 XX
 PT Compens. contg. DP-178 or DP-107 in combination with other therapeutic
 PT agent - useful for treatment of HIV infection, esp. by inhibiting
 PT replication or transmission of HIV.
 XX
 PS Claim 2; Fig 1; 84pp; English.
 XX
 CC AAM17011 represents a peptide designated DP-178, a peptide derived from
 CC HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The peptide
 CC corresponds to residues 638-673 of gp41. DP-178 and its derivatives are
 CC used in combination with a therapeutic agent, e.g. a reverse
 CC transcriptase, viral protease, cytokine, glycosylation or viral RNA
 CC processing inhibitor or a nucleoside inhibitor. The peptides work by
 CC inhibiting viral replication or inhibiting transmission. They may also be
 CC used in vaccines for protecting against HIV infection. (Updated on 17-OCT
 CC -2003 to standardise OS field)
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLSLHSLIESQNOQEKNEQELLEDKVASLWNMF 36
 DB 1 YTSLSLHSLIESQNOQEKNEQELLEDKVASLWNMF 36
 RESULT 4
 AAY22912
 ID AAY22912 standard; peptide; 36 AA.
 XX
 AC AAY22912;
 XX
 DT 19-AUG-1999 (first entry)
 DT
 XX
 DE SEQ ID NO. 108 from WO9820036.

XX HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
 KW antibody; viral membrane fusion; viral infectivity;
 KW ligand affinity purification; protein A replacement;
 KW immunoglobulin purification; epitope mimic.
 OS Human immunodeficiency virus.
 XX MO9820036-A1.
 PN 14-MAY-1998.
 XX PD 05-NOV-1997; 97WO-US020069.
 XX PF 06-NOV-1996; 96US-00743698.
 XX PR 16-JUN-1997; 97US-00876698.
 XX PA (GETH) GENENTECH INC.
 XX PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX WPI; 1998-286866/25.
 DR WPI; 1998-286866/25.
 XX PT Production of constrained helical peptide(s) by linking side chains on
 PT termini of octa-peptide - derived from human immunodeficiency virus gp41
 PT protein, useful in vaccines for treatment and prevention of infection.
 XX PS Disclosure; Page 233-234, 279pp; English.
 XX XX
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
 CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
 CC AAY22903 represent consensus sequences of various sections of the gp41
 CC protein). Sequences derived from the peptides are used to produce
 CC constrained helical peptides of the invention. The constrained helical
 CC peptide is produced by synthesizing an octapeptide in which both terminal
 CC amino acids have a side-chain that includes a group able to form an amide
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification); as
 CC epitope mimics for antibody production; for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 XX SQ Sequence 36 AA;
 XX
 QY Query Match 100.0%; Score 36; DB 2; Length 36;
 Db Best Local Similarity 100.0%; Pred. No. 1.4e-28; Mismatches 0; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 YTSLSLSLIESQNOQEKNEQBELLELDKMASLWNMF 36
 1 YTSLSLSLIESQNOQEKNEQBELLELDKMASLWNMF 36
 Db 1 YTSLSLSLIESQNOQEKNEQBELLELDKMASLWNMF 36
 RESULT 5
 AAY22805
 ID AAY22805 standard; peptide; 36 AA.
 XX
 AC AAY22805;
 XX
 XX 19-AUG-1999 (first entry)
 DT
 XX SEQ ID NO. 1 from WO9820036.
 DE
 XX

KW HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
 KW antibody; viral membrane fusion; viral infectivity;
 KW ligand affinity purification; protein A replacement;
 KW immunoglobulin purification; epitope mimic.
 OS Human immunodeficiency virus.
 XX MO9820036-A1.
 PN 14-MAY-1998.
 XX PD 05-NOV-1997; 97WO-US020069.
 XX PF 06-NOV-1996; 96US-00743698.
 XX PR 16-JUN-1997; 97US-00876698.
 XX PA (GETH) GENENTECH INC.
 XX PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX WPI; 1998-286866/25.
 DR WPI; 1998-286866/25.
 XX PT Production of constrained helical peptide(s) by linking side chains on
 PT termini of octa-peptide - derived from human immunodeficiency virus gp41
 PT protein, useful in vaccines for treatment and prevention of infection.
 XX PS Disclosure; Page 143-144, 279pp; English.
 XX XX
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
 CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
 CC AAY22903 represent consensus sequences of various sections of the gp41
 CC protein). Sequences derived from the peptides are used to produce
 CC constrained helical peptides of the invention. The constrained helical
 CC peptide is produced by synthesizing an octapeptide in which both terminal
 CC amino acids have a side-chain that includes a group able to form an amide
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification); as
 CC epitope mimics for antibody production; for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 XX SQ Sequence 36 AA;
 XX
 QY Query Match 100.0%; Score 36; DB 2; Length 36;
 Db Best Local Similarity 100.0%; Pred. No. 1.4e-28; Mismatches 0; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 YTSLSLSLIESQNOQEKNEQBELLELDKMASLWNMF 36
 1 YTSLSLSLIESQNOQEKNEQBELLELDKMASLWNMF 36
 Db 1 YTSLSLSLIESQNOQEKNEQBELLELDKMASLWNMF 36
 RESULT 6
 AAY1974
 ID AAY1974 standard; peptide; 36 AA.
 XX
 AC AAY1974;
 XX
 XX 17-OCT-2003 (revised)
 DT
 XX 21-DEC-1999 (first entry)
 DT
 XX HIV-1 LAI gp41 T-20 peptide.
 DE
 XX

KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN MO9948513-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99WO-US006230.
 XX
 PR 23-MAR-1998; 98US-00045920.
 PR 01-MAY-1998; 98US-00071877.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Kang M, Bray B, Lichty M, Mader C, Merutka G;
 XX
 DR WPI; 1999-591038/50.
 XX
 PT Methods of peptide synthesis, particularly used to produce T-20 or T-20
 PT like peptides.
 XX
 PS Disclosure; Page 9; 120pp; English.
 XX
 CC The present sequence represents a peptide, designated T-20 (or DP-178),
 CC that corresponds to amino acids 638-673 of the transmembrane protein gp41
 CC of HIV-1 LAI isolate. The invention relates to methods for the synthesis
 CC of peptides, in particular C- and N-terminal modified T-20 (see AAY31955)
 CC and T-20-like peptides. The method involves synthesizing specific side-
 CC chain protected peptide fragment intermediates (see AAY31956-73) of T-20
 CC or a T-20-like peptide on a solid support, coupling the protected
 CC fragments in solution to form a protected T-20 or T-20-like peptide,
 CC followed by deprotection of the side chains to yield the final T-20 or T-
 CC 20-like peptide. The invention also relates to individual peptide
 CC fragments which act as intermediates in the synthesis of peptides of
 CC interest (e.g. T-20), and to particular groups of peptide fragments which
 CC act as intermediates in the synthesis of the peptide of interest. The
 CC method allows for the large scale, economical production of high purity
 CC peptides. (Updated on 17-Oct-2003 to standardise OS field)
 CC
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLNNMF 36
 DB 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLNNMF 36
 RESULT 7
 AAY31955
 ID AAY31955 standard; peptide; 36 AA.
 AC AAY31955;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Synthetic peptide T-20 (DP-178).
 XX
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site /note= "N-terminal acetyl"
 FT Modified-site 36
 FT /note= "C-terminal amide"
 XX
 PN MO9948513-A1.

XX
 PD 30-SEP-1999.
 XX
 PF 22-MAR-1999; 99WO-US006230.
 XX
 PR 23-MAR-1998; 98US-00045920.
 PR 01-MAY-1998; 98US-00071877.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Kang M, Bray B, Lichty M, Mader C, Merutka G;
 XX
 DR WPI; 1999-591038/50.
 XX
 PT Methods of peptide synthesis, particularly used to produce T-20 or T-20
 PT like peptides.
 XX
 PS Claim 1; Page 102; 120pp; English.
 XX
 CC The present sequence represents an N- and C-terminal modified peptide,
 CC designated T-20 (or DP-178), corresponding to amino acids 638-673 of the
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention relates to
 CC methods for the synthesis of peptides, in particular T-20 and T-20-like
 CC peptides. The method involves synthesizing specific side-chain protected
 CC peptide fragment intermediates of T-20 or a T-20-like peptide on a solid
 CC support, coupling the protected fragments in solution to form a protected
 CC T-20 or T-20-like peptide, followed by deprotection of the side chains to
 CC yield the final T-20 or T-20-like peptide. The invention also relates to
 CC individual peptide fragments (see AAY31956-73) which act as intermediates
 CC in the synthesis of peptides of interest (e.g. T-20), and to particular
 CC groups of peptide fragments which act as intermediates in the synthesis
 CC of the peptide of interest. The method allows for the large scale,
 CC economical production of high purity peptides
 CC
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 36; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLNNMF 36
 DB 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLNNMF 36
 RESULT 8
 AAY89999
 ID AAY89999 standard; peptide; 36 AA.
 AC AAY89999;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Core polypeptide fragment T No. 1598.
 XX
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KW anti-fusogenic; differentiation factor; interleukin; interferon;
 KW colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 OS
 PN WO9959615-A1.
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US011219.
 XX
 PR 20-MAY-1998; 98US-00082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
PS Disclosure; Page 48; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36
1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36
Db

RESULT 9

AAY8665
ID AAY8665 standard; peptide; 36 AA.

AC AAY8665;

DT 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 20.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO9595615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

XX Disclosure; Page 21; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide

CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

OY 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36
1 YTSLSHSLIESQNOQEKNEQELLEDKMASLWNMF 36
Db

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAY89777;

DT 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 1343.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO9595615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US011219.

PR 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.

XX Disclosure; Page 44; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAY8651-Y9005 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36
1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36
DB 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36

RESULT 11

AAY89982
ID AAY89982 standard; peptide; 36 AA.

AC AAY89982;

XX 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 1559.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

XX WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.

XX Disclosure; Page 48; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAY8651-Y9005 represent core polypeptide fragments that can
XX be used in the invention. Some sequences among those indicated also
XX comprise enhancer fragments at terminal ends and form hybrid polypeptides
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36
1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36
DB 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36

RESULT 12

AAY89424
ID AAY89424 standard; peptide; 36 AA.

AC AAY89424;

XX 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 974.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
XX anti-fusogenic; differentiation factor; interleukin; interferon;
XX colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

XX WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US011219.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties
XX comprises enhancer sequence.

XX Disclosure; Page 36; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide
XX sequence linked to core polypeptides. The enhancer polypeptides are
XX derived from various retroviral envelope (gp41) protein sequences,
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX pharmacokinetic properties such as increasing the half-life of any core
XX polypeptide that they are linked to. The core polypeptides are any
XX polypeptide that may be introduced into a living system and that can
XX function as a pharmacologically useful peptide for the treatment or
XX prevention of a disease. The core polypeptides are bioactive peptides
XX selected from a growth factor, cytokine, differentiation factor,
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic
XX factor. The peptides of the invention can be used for inhibiting viral
XX infection and can be used in anti-viral and anti-fusogenic treatments.
XX Sequences AAY8651-Y9005 represent core polypeptide fragments that can
XX be used in the invention. Some sequences among those indicated also
XX comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36
1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36
DB 1 YTSLSHSLIESQNOQEKNEQELLEDKMASLMMWF 36

```

RESULT 13
AAV89692
ID AAV89692 standard; peptide; 36 AA.
XX
AC AAV89692;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 1254.
XX
KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN W09959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99MO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
PS Disclosure; Page 42; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAV8651-Y90055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
CC
XX
SQ Sequence 36 AA;
XX
Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIESONQOEKNEQLLELDKMASLWNMF 36
DB 1 YTSLSHSLIESONQOEKNEQLLELDKMASLWNMF 36
XX
RESULT 14
AAV89242
ID AAV89242 standard; peptide; 36 AA.
XX
AC AAV89242;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 680.
XX

```

```

XX
KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN W09959615-A1.
XX
PD 25-NOV-1999.
XX
PF 20-MAY-1999; 99MO-US011219.
XX
PR 20-MAY-1998; 98US-00082279.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX
DR WPI; 2000-136792/12.
XX
PT A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
PS Disclosure; Page 32; 124pp; English.
XX
CC The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-fusogenic treatments.
CC Sequences AAV8651-Y90055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
CC
XX
SQ Sequence 36 AA;
XX
Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIESONQOEKNEQLLELDKMASLWNMF 36
DB 1 YTSLSHSLIESONQOEKNEQLLELDKMASLWNMF 36
XX
RESULT 15
AAV89983
ID AAV89983 standard; peptide; 36 AA.
XX
AC AAV89983;
XX
DT 23-MAY-2000 (first entry)
XX
DE Core polypeptide fragment T No. 1563.
XX
KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KM anti-fusogenic; differentiation factor; interleukin; interferon;
KM colony stimulating factor; hormone; angiogenic factor.
XX
OS Unidentified.
XX
PN W09959615-A1.
XX

```

XX 25-NOV-1999.
PD
XX
XX 20-MAY-1999; 99WO-US011219.
PF
XX
XX 20-MAY-1998; 98US-00082279.
PR
XX
XX (TRIM-) TRIMERIS INC.
PA
XX
XX Barney S, Guthrie KI, Merutka G, Auwer MK, Lambert DM;
PI
XX WPI; 2000-136792/12.
DR
XX
XX A new hybrid polypeptide with enhanced pharmacokinetic properties
PT comprises enhancer sequence.
XX
XX
PS Disclosure; Page 48; 124pp; English.
XX
XX The invention relates to hybrid polypeptides comprising enhancer peptide
CC sequence linked to core polypeptides. The enhancer polypeptides are
CC derived from various retroviral envelope (gp41) protein sequences,
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
CC pharmacokinetic properties such as increasing the half-life of any core
CC polypeptide that they are linked to. The core polypeptides are any
CC polypeptide that may be introduced into a living system and that can
CC function as a pharmacologically useful peptide for the treatment or
CC prevention of a disease. The core polypeptides are bioactive peptides
CC selected from a growth factor, cytokine, differentiation factor,
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic
CC factor. The peptides of the invention can be used for inhibiting viral
CC infection and can be used in anti-viral and anti-tumorigenic treatments.
CC Sequences AY88651-Y90055 represent core polypeptide fragments that can
CC be used in the invention. Some sequences among those indicated also
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides
XX
SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.4e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLFEESQNOQEKNOELLELDKVASLNMWF 36
Db 1 YTSLSHSLFEESQNOQEKNOELLELDKVASLNMWF 36

Search completed: September 20, 2005, 19:55:06
Job time : 168 secs


```

VCLJH3
env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Joseph, S.F.; Doranberger, J.A.; Papae, T.S.; Grayer, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 100.0%; Score 36; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 4,1e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLMMNF 36
Db 638 YTSLSHSLIESONQOEKNEQELLELDKWSLMMNF 673

RESULT 4
VCLJIV
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allison, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAT>
A:Cross-references: UNIPROT:P03377; GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 100.0%; Score 36; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 4,2e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLMMNF 36
Db 643 YTSLSHSLIESONQOEKNEQELLELDKWSLMMNF 678

RESULT 5
VCLJVL
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)

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```

N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03974
R:Neueing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laeky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUR>
A:Cross-references: UNIPROT:P03376; GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 83.3%; Score 30; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3,9e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESONQOEKNEQELLELDKWA 30
Db 638 YTSLSHSLIESONQOEKNEQELLELDKWA 667

RESULT 6
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determin
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STB1>
A:Cross-references: UNIPROT:Q78118; EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polypeptide

Query Match 80.6%; Score 29; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 1,8e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LIESONQOEKNEQELLELDKWSLMMNF 36
Db 146 LIESONQOEKNEQELLELDKWSLMMNF 174

RESULT 7
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70422; S21996

```


R;Steuler, H.; Storch-Hagenlocher, B.; Willemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
 A;Reference number: S70417, MUID:92144209, PMID:1736940
 A;Accession: S70422
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-357 <ST2>
 A;Cross-references: UNIPROT:Q78119; EMBL:X61356; NID:960181; PIDN:CAA3624.1; PID:G10671
 A;Experimental source: patient 27L
 A;Note: submitted to the EMBL Data Library, July 1991
 C;Superfamily: type B retrovirus env polypeptide

Query Match 80.6%; Score 29; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.8e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIBESONQOEKNEQELLEDKMASLWNMF 36
 |||||
 Db 146 LIBESONQOEKNEQELLEDKMASLWNMF 174

RESULT 8

C41621
 env polypeptide P - human immunodeficiency virus type 1 (fragment)
 N;Alternate names: coat polypeptide
 N;Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)
 C;Accession: C41621
 R;Burger, H.; Weiser, B.; Flaherty, K.; Gupta, J.; Nguyen, P.N.; Gibbc, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A;Reference number: A41621; MUID:92107924; PMID:1763038

A;Accession: C41621
 A;Molecule type: DNA

A;Residues: 1-443 <BUR>

A;Cross-references: UNIPROT:Q80023; GB:M77230; NID:G328631; PIDN:AAB03792.1; PID:G555015
 A;Note: this virus was isolated from the mother's sexual partner

C;Genetics:

A;Gene: env
 C;Superfamily: type B retrovirus env polypeptide

C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
 F;1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F;52-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F;424-443/Domain: transmembrane #status predicted <TM>

F;9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 80.6%; Score 29; DB 2; Length 443;
 Best Local Similarity 100.0%; Pred. No. 2.1e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIBESONQOEKNEQELLEDKMASLWNMF 36
 |||||
 Db 385 LIBESONQOEKNEQELLEDKMASLWNMF 413

RESULT 9

T09448
 envelope glycoprotein - human immunodeficiency virus type 1 (strain JRL)

C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T09448
 R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
 submitted to the EMBL Data Library, July 1996

A;Reference number: Z16673
 A;Accession: T09448

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA
 A;Residues: 1-847 <PAN>

A;Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:G1465777; PID:G1465781
 C;Genetics:

A;Gene: env
 C;Superfamily: type B retrovirus env polypeptide

Query Match 80.6%; Score 29; DB 2; Length 847;
 Best Local Similarity 100.0%; Pred. No. 3.9e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIBESONQOEKNEQELLEDKMASLWNMF 36
 |||||
 Db 636 LIBESONQOEKNEQELLEDKMASLWNMF 664

RESULT 10

S13289
 env polypeptide - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S13289
 R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
 Nature 348, 69-73, 1990
 A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
 A;Reference number: S13288; MUID:91043044; PMID:2172833

A;Accession: S13289

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-847 <OBR>

A;Cross-references: UNIPROT:Q75760
 C;Superfamily: type B retrovirus env polypeptide

Query Match 80.6%; Score 29; DB 2; Length 847;
 Best Local Similarity 100.0%; Pred. No. 3.9e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIBESONQOEKNEQELLEDKMASLWNMF 36
 |||||
 Db 636 LIBESONQOEKNEQELLEDKMASLWNMF 664

RESULT 11

VCLJ3W
 env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
 C;Accession: A24774

R;Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986

A>Title: Identification and characterization of conserved and variable regions in the env
 A;Reference number: A24774; MUID:86218077; PMID:2423250

A;Accession: A24774

A;Molecule type: DNA

A;Residues: 1-856 <STA>

A;Cross-references: UNIPROT:P31872; GB:K03455; GB:M34432; NID:G1906382

C;Genetics:

A;Gene: env
 C;Superfamily: type B retrovirus env polypeptide

C;Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-501/Product: coat protein gp120 #status predicted <GP1>
 F;502-847/Product: coat protein gp41 #status predicted <GP2>

F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,
 487,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000

Query Match 80.6%; Score 29; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3.9e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIBESONQOEKNEQELLEDKMASLWNMF 36
 |||||
 Db 645 LIBESONQOEKNEQELLEDKMASLWNMF 673

RESULT 12

VCLJ3C

```
env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Guigou, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Gene: env
C:Genetics:
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polypeptide #status predicted <ERP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
Query Match 80.6%; Score 29; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 3.9e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIEESONQOEKNEBELLELDKWSLWNMF 36
DB 650 LIEESONQOEKNEBELLELDKWSLWNMF 678

RESULT 13
env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.V.; Steimer, K.S.; Stempien, M.M.; Brown-SH
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453; PMID:2578227
A:Accession: A03976
A:Molecule type: DNA
A:Residues: 1-855 <SAN>
A:Cross-references: UNIPROT:P03378; GB:K02007; NID:G328658; PIDN:AAB59882.1; PID:G328666
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,158,164,190,200,244,265,297,298,304,334,341,358,364,388,394,400,408,445,458
F:610,624,636,615/binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.0%; Score 27; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEBELLELDKWSLWNMF 36
DB 646 EESONQOEKNEBELLELDKWSLWNMF 672

RESULT 14
S21998
env polypeptide gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
```

```
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STB1>
A:Cross-references: UNIPROT:078120; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STB2>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
C:Superfamily: type E retrovirus env polypeptide

Query Match 69.4%; Score 25; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SONQOEKNEBELLELDKWSLWNMF 36
DB 151 SONQOEKNEBELLELDKWSLWNMF 175

RESULT 15
env polypeptide gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70424; S21992
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70424
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:078112; EMBL:X61358; NID:g60177; PIDN:CAA43628.1; PID:g60178
A:Experimental source: patient 22
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide

Query Match 61.1%; Score 22; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SONQOEKNEBELLELDKWSLWNMF 33
DB 150 SONQOEKNEBELLELDKWSLWNMF 171

Search completed: September 20, 2005, 19:58:48
Job time : 41 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2005, 19:47:51 ; Search time 169 Seconds
(without alignments)
109.082 Million cell updates/sec

Title: US-09-809-060A-1
Perfect score: 36
Sequence: 1 YTSLIHSLIESQNOQKNEQELLELDKMASLWNMF 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	645	Q993A6	Q993A6 human immun
2	36	100.0	747	Q70607	Q70607 human immun
3	36	100.0	748	Q70606	Q70606 human immun
4	36	100.0	752	Q70604	Q70604 human immun
5	36	100.0	752	Q70605	Q70605 human immun
6	36	100.0	752	Q70608	Q70608 human immun
7	36	100.0	851	ENV_HV1B8	P04582 human immun
8	36	100.0	851	Q78243	Q78243 human immun
9	36	100.0	852	Q6TAP8	Q6TAP8 human immun
10	36	100.0	852	Q6TAP9	Q6TAP9 human immun
11	36	100.0	852	Q6TAQ1	Q6TAQ1 human immun
12	36	100.0	852	Q6TAQ2	Q6TAQ2 human immun
13	36	100.0	852	Q6TAQ3	Q6TAQ3 human immun
14	36	100.0	852	Q6TAQ4	Q6TAQ4 human immun
15	36	100.0	852	Q6TAP5	Q6TAP5 human immun
16	36	100.0	852	Q6TAP6	Q6TAP6 human immun
17	36	100.0	854	Q6BIC6	Q6BIC6 human immun
18	36	100.0	854	Q6TAN3	Q6TAN3 human immun
19	36	100.0	854	Q6TAN4	Q6TAN4 human immun
20	36	100.0	854	Q6TAN5	Q6TAN5 human immun
21	36	100.0	854	Q6TAN6	Q6TAN6 human immun
22	36	100.0	854	Q6TAN7	Q6TAN7 human immun
23	36	100.0	854	Q6TAN8	Q6TAN8 human immun
24	36	100.0	854	Q72502	Q72502 human immun
25	36	100.0	854	Q6S582	Q6S582 human immun
26	36	100.0	856	ENV_HV1B1	P03375 human immun
27	36	100.0	856	ENV_HV1B2	P04578 human immun
28	36	100.0	856	ENV_HV1B3	P04624 human immun
29	36	100.0	856	ENV_HV1LW	Q70626 human immun
30	36	100.0	856	Q92877	Q92877 simian-huma
31	36	100.0	856	Q74090	Q74090 human immun

32	36	100.0	856	2	Q74599	human immun
33	36	100.0	861	1	ENV_HV1B8	human immun
34	35	97.2	616	2	Q993B0	human immun
35	35	97.2	618	2	Q993B2	human immun
36	30	83.3	122	2	Q6DL73	human immun
37	30	83.3	122	2	Q6V8Y9	human immun
38	30	83.3	122	2	Q9Q1W0	human immun
39	30	83.3	809	2	Q6QL15	human immun
40	30	83.3	838	2	Q03806	human immun
41	30	83.3	847	2	Q72BZ0	human immun
42	30	83.3	848	2	Q69990	human immun
43	30	83.3	853	2	Q6BC11	human immun
44	30	83.3	854	2	Q78225	human immun
45	30	83.3	855	2	Q03805	human immun

ALIGNMENTS

```
RESULT 1
Q993A6 PRELIMINARY; PRT; 645 AA.
AC Q993A6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Truncated envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MBLINB=21192672; PubMed=11287644; DOI=10.1073/pnas.071063898;
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,
RA White S.W., Doherty P.C., Hurwitz J.L.;
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of
RT HIV envelope glycoprotein suggests structural influences on antigen
RT processing".
RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).
DR EMBL; AF321563; AAK18810.1; -.
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER
SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362BC CRC64;

Query Match 100.0%; Score 36; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 8.9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHSLIESQNOQKNEQELLELDKMASLWNMF 36
Db 607 YTSLIHSLIESQNOQKNEQELLELDKMASLWNMF 642

RESULT 2
Q70607 PRELIMINARY; PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
```

QY	DB	SEQUENCE	Match	Similarity	Score	DB 2	Length	747	Gaps
QY	DB	1 YTSLSHSLSIESNQKNEBELLELDKMASLMMWF 36	100.0%	100.0%	36	DB 2	747		0
DB		633 YTSLSHSLSIESNQKNEBELLELDKMASLMMWF 668	36	Conservative	0	Mismatches	0	Indels	0
<p>Query Match</p> <p>Best Local Similarity 100.0%; Score 36; DB 2; Length 747;</p> <p>Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>									
<p>RESULT 3</p> <p>Q70606 PRELIMINARY; PRT; 748 AA.</p> <p>Q70606</p> <p>01-NOV-1996 (TREMBLrel. 01, Created)</p> <p>01-NOV-1996 (TREMBLrel. 01, Last sequence update)</p> <p>01-JUN-2003 (TREMBLrel. 24, Last annotation update)</p> <p>Envelope glycoprotein (Fragment).</p> <p>GN Name-env;</p> <p>OS Human immunodeficiency virus 1.</p> <p>OC Viruses; Retroid viruses; Retroviridae; Lentivirus.</p> <p>OX NCBI_TaxID=11676;</p> <p>RN [1]</p> <p>RN SEQUENCE FROM N.A.</p> <p>RA MEDLINE=95127297; PubMed=7826699;</p> <p>RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,</p> <p>RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;</p> <p>RT "viral variability and serum antibody response in a laboratory worker</p> <p>RT infected with HIV type 1 (HTLV type IIB).";</p> <p>RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).</p> <p>RN [2]</p> <p>RN SEQUENCE FROM N.A.</p> <p>RP Mulder K.E.;</p> <p>RA Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.</p> <p>RL EMBL; U12032; AAA76668.1; -.</p> <p>DR PIR; A53591; A53591.</p> <p>DR HSSP; P04578; IAIK.</p> <p>DR GO; GO:0016021; C:Integral to membrane; IEA.</p> <p>DR GO; GO:0019028; C:viral capsid; IEA.</p> <p>DR GO; GO:0019031; C:viral envelope; IEA.</p> <p>DR GO; GO:0005198; F:structural molecule activity; IEA.</p> <p>DR InterPro; IPR000328; Env GP41.</p> <p>DR InterPro; IPR000777; GP120.</p> <p>DR PIR; A53591; A53591.</p> <p>DR HSSP; P04578; IAIK.</p> <p>DR GO; GO:0016021; C:Integral to membrane; IEA.</p> <p>DR GO; GO:0019028; C:viral capsid; IEA.</p> <p>DR GO; GO:0019031; C:viral envelope; IEA.</p> <p>DR GO; GO:0005198; F:structural molecule activity; IEA.</p> <p>DR InterPro; IPR000328; Env GP41.</p> <p>DR InterPro; IPR000777; GP120.</p>									

```

DR PFam: PF00516; GP120; 1.
DR PFam: PF00517; GP41; 1.
KM AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
transmembrane.
FT NON_TER 748 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 36; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIBSONQOEKNEBELLELDKMSLWNMF 36
|||||
Db 634 YTSLSHLSIBSONQOEKNEBELLELDKMSLWNMF 669

RESULT 4
Q70604 PRELIMINARY; PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; Pubmed=7826699.
RA Reltz M., Hall U., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type 1)"
RL AIDS Res. Hum. Retroviruses 10:1143-1155 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RL Mulder K.E.;
DR Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AAA7666.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR PFam; PF00516; GP120; 1.
DR PFam; PF00517; GP41; 1.
KM AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
transmembrane.
FT NON_TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AEB94013B45A CRC64;

Query Match 100.0%; Score 36; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIBSONQOEKNEBELLELDKMSLWNMF 36
|||||
Db 638 YTSLSHLSIBSONQOEKNEBELLELDKMSLWNMF 673

RESULT 5
Q70605 PRELIMINARY; PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).

```

```

GN Name=env;
OC Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AAA7667.1; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
  Transmembrane.
KW Transmembrane.
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 36; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDKMASLMMWF 36
Db 638 YTSLSHLSIESQNOQEKNEQELLEDKMASLMMWF 673

RESULT 6
ID Q70608 PRELIMINARY; PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12035; AAA7667.0; -.
DR PIR; A53591; A53591.
DR HSSP; P04578; 1A1K.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.

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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
  Transmembrane.
KW Transmembrane.
SQ SEQUENCE 752 AA; 84779 MW; 708672A2D0C0E8F8 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDKMASLMMWF 36
Db 638 YTSLSHLSIESQNOQEKNEQELLEDKMASLMMWF 673

RESULT 7
ID ENV_HY1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN Name=ENV;
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W.A., Patarca R., Lyak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Ratajski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
CC CC
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CC CC
DR EMBL; K02011; AAA44661.1; -.
DR PDB; 1DDH; X-ray; P=311-320.
DR PDB; 1HHG; X-ray; C/P=192-200.
DR PDB; 1QO3; X-ray; P=311-320.
DR PDB; 1S2T; X-ray; @=541-650.
DR GLYCOSUB; P04582; -.
DR HIV; K02011; ENV5B8H.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW 3D-structure; AIDS; Coat protein; Glycoprotein; Polyprotein; Signal;
  Transmembrane.
FT SIGNAL 1 30
FT CHAIN 31 506 Exterior membrane glycoprotein.
FT CHAIN 507 851 Transmembrane glycoprotein.
FT DISULFID 54 74 By similarity.
FT DISULFID 119 205 By similarity.
FT DISULFID 126 196 By similarity.
FT DISULFID 131 157 By similarity.
FT DISULFID 216 247 By similarity.
FT DISULFID 228 239 By similarity.
FT DISULFID 296 331 By similarity.
FT DISULFID 378 440 By similarity.

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FT DISUFLD 385 413 By similarity.
FT CARBOHYD 88 88 N-linked (GlcNAc...) (potential).
FT CARBOHYD 136 136 N-linked (GlcNAc...) (potential).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (potential).
FT CARBOHYD 156 156 N-linked (GlcNAc...) (potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (potential).
FT CARBOHYD 186 186 N-linked (GlcNAc...) (potential).
FT CARBOHYD 197 197 N-linked (GlcNAc...) (potential).
FT CARBOHYD 230 230 N-linked (GlcNAc...) (potential).
FT CARBOHYD 234 234 N-linked (GlcNAc...) (potential).
FT CARBOHYD 241 241 N-linked (GlcNAc...) (potential).
FT CARBOHYD 262 262 N-linked (GlcNAc...) (potential).
FT CARBOHYD 276 276 N-linked (GlcNAc...) (potential).
FT CARBOHYD 295 295 N-linked (GlcNAc...) (potential).
FT CARBOHYD 301 301 N-linked (GlcNAc...) (potential).
FT CARBOHYD 332 332 N-linked (GlcNAc...) (potential).
FT CARBOHYD 339 339 N-linked (GlcNAc...) (potential).
FT CARBOHYD 356 356 N-linked (GlcNAc...) (potential).
FT CARBOHYD 386 386 N-linked (GlcNAc...) (potential).
FT CARBOHYD 392 392 N-linked (GlcNAc...) (potential).
FT CARBOHYD 401 401 N-linked (GlcNAc...) (potential).
FT CARBOHYD 443 443 N-linked (GlcNAc...) (potential).
FT CARBOHYD 458 458 N-linked (GlcNAc...) (potential).
FT CARBOHYD 606 606 N-linked (GlcNAc...) (potential).
FT CARBOHYD 611 611 N-linked (GlcNAc...) (potential).
FT CARBOHYD 620 620 N-linked (GlcNAc...) (potential).
FT CARBOHYD 632 632 N-linked (GlcNAc...) (potential).
FT CARBOHYD 669 669 N-linked (GlcNAc...) (potential).
FT CARBOHYD 745 745 N-linked (GlcNAc...) (potential).
FT CARBOHYD 811 811 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
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Query Match 100.0%; Score 36; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 YTSLSHLSIESONOEKNEQLLELDKXASIMNMF 36
Db 633 YTSLSHLSIESONOEKNEQLLELDKXASIMNMF 668
```

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RESULT 8
O78243 PRELIMINARY; PRT; 851 AA.
AC O78243;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Env polyprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69352106; PubMed=2765297;
RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
RT producer clones from HUT-78 infected with a patient HIV isolate.";
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Boretto A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
RT productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
RN [3]
RP SEQUENCE FROM N.A.
RA Carlini F., Federico M., Equestre M., Ricci S., Ratti G., Zibai Q.,
RA Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
```

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RT chronically infected HUT-78 cellular clone.";
RL J. Viral Dis. 1:40-55(1992).
DR EMBL; Z11530; CAAT7628.1; -.
DR PIR; A53591; A53591.
DR PIR; S13288; S13288.
DR PIR; S33985; S33985.
DR HSSP; P04578; IAIK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 851 AA; 96629 MW; 1A37679B7E98027 CRC64;
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Query Match 100.0%; Score 36; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 YTSLSHLSIESONOEKNEQLLELDKXASIMNMF 36
Db 633 YTSLSHLSIESONOEKNEQLLELDKXASIMNMF 668
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RESULT 9
O6TAP8 PRELIMINARY; PRT; 852 AA.
AC O6TAP8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor
RT Switching.";
RL J. Virol. 78:7565-7574(2004).
DR EMBL; AY426107; AAR05831.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96903 MW; 3F5B7D44DBE6BFBC CRC64;
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Query Match 100.0%; Score 36; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 YTSLSHLSIESONOEKNEQLLELDKXASIMNMF 36
Db 634 YTSLSHLSIESONOEKNEQLLELDKXASIMNMF 669
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RESULT 10
O6TAP9 PRELIMINARY; PRT; 852 AA.
AC O6TAP9;
DT 06TAP9;
DT 06TAP9;
DT 06TAP9;
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DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Envelope glycoprotein.
CN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426108; AAR05832.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KM Transmembrane.
SQ SEQUENCE 852 AA; 96971 MW; 1E186A2DEDS0F57E CRC64;

Query Match 100.0%; Score 36; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 36
Db 634 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 669

RESULT 11
Q6TAAQ1
ID O6TAAQ1 PRELIMINARY; PRT; 852 AA.
AC O6TAAQ1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Envelope glycoprotein.
CN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426108; AAR05830.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KM Transmembrane.
SQ SEQUENCE 852 AA; 97001 MW; 8DF59CAUD8AC145E CRC64;

Query Match 100.0%; Score 36; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 36
Db 634 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 669

RESULT 12
Q6TAAQ2
ID O6TAAQ2 PRELIMINARY; PRT; 852 AA.
AC O6TAAQ2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Envelope glycoprotein.
CN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426105; AAR05829.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KM Transmembrane.
SQ SEQUENCE 852 AA; 96862 MW; E9D1E7BE8CD93B12 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 36
Db 634 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 669

RESULT 13
Q6TAAQ3
ID O6TAAQ3 PRELIMINARY; PRT; 852 AA.
AC O6TAAQ3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Envelope glycoprotein.
CN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C., Ramos A., Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching."
RL J. Virol. 78:7565-7574(2004).
EMBL: AY426104; AAR05828.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.

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DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96835 MW; 92EB22A98CD9316 CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 852;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLELDKMASLWNMF 36
DB 634 YTSLSHSLIESQNOEKNEQELLELDKMASLWNMF 669

RESULT 14
Q6TA04 PRELIMINARY; PRT; 852 AA.
AC O6TA04;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C.; Ramos A.; Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor Switching.";
RL J. Virol. 78:7565-7574(2004).
DR EMBL; AY426103; AAR05827.1; -.
DR HSSP; P04578; 1AIR.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96860 MW; 62B200F64D5D4F7A CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 852;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLELDKMASLWNMF 36
DB 634 YTSLSHSLIESQNOEKNEQELLELDKMASLWNMF 669

RESULT 15
Q6TA05 PRELIMINARY; PRT; 852 AA.
AC O6TA05;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15220431; DOI=10.1128/JVI.78.14.7565-7574.2004;
RA Pastore C.; Ramos A.; Mosier D.E.;
RT "Intrinsic Obstacles to Human Immunodeficiency Virus Type 1 Coreceptor

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RT Switching.";
RL J. Virol. 78:7565-7574(2004).
DR EMBL; AY426102; AAR05826.1; -.
DR HSSP; P04578; 1AIR.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96860 MW; 62B201D94FC1FF7A CRC64;

Query Match
Best Local Similarity 100.0%; Score 36; DB 2; Length 852;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLELDKMASLWNMF 36
DB 634 YTSLSHSLIESQNOEKNEQELLELDKMASLWNMF 669

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Search completed: September 20, 2005, 19:58:01
Job time : 170 secs

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OM protein - protein search, using sw model

Run on: September 20, 2005, 19:49:26 / Search time 42 Seconds
(without alignments)
63.985 Million cell updates/sec

Title: US-09-809-060A-1

Perfect score: 36

Sequence: 1 YTSLSHSLIESQNOQEKNEQLELDKMSLWNMF 36

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A COMB .pep:.*
2: /cgn2_6/ptodata/1/1aa/5B COMB .pep:.*
3: /cgn2_6/ptodata/1/1aa/6A COMB .pep:.*
4: /cgn2_6/ptodata/1/1aa/6B COMB .pep:.*
5: /cgn2_6/ptodata/1/1aa/PCUS COMB .pep:.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pcp:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	36	1	US-08-073-028-1
2	36	100.0	36	3	US-08-486-099-1
3	36	100.0	36	3	US-09-071-877-1
4	36	100.0	36	3	US-08-360-107A-1
5	36	100.0	36	3	US-08-484-323B-1
6	36	100.0	36	3	US-08-919-597-1
7	36	100.0	36	3	US-08-475-668A-1
8	36	100.0	36	3	US-08-485-551A-1
9	36	100.0	36	3	US-08-471-913A-1
10	36	100.0	36	3	US-08-554-616-1
11	36	100.0	36	3	US-08-485-264A-1
12	36	100.0	36	3	US-09-082-279B-15
13	36	100.0	36	3	US-09-082-279B-497
14	36	100.0	36	3	US-09-082-279B-498
15	36	100.0	36	3	US-09-082-279B-603
16	36	100.0	36	3	US-09-082-279B-630
17	36	100.0	36	3	US-09-082-279B-631
18	36	100.0	36	3	US-09-082-279B-705
19	36	100.0	36	3	US-09-082-279B-834
20	36	100.0	36	3	US-09-082-279B-1076
21	36	100.0	36	3	US-09-082-279B-1121
22	36	100.0	36	3	US-09-082-279B-1161
23	36	100.0	36	3	US-08-965-056-1
24	36	100.0	36	3	US-08-965-056-108
25	36	100.0	36	3	US-09-045-520-1
26	36	100.0	36	3	US-08-474-349A-1
27	36	100.0	36	3	US-08-474-349A-399

28	36	100.0	36	3	US-08-474-349A-413	Sequence 413, App
29	36	100.0	36	3	US-09-315-304B-15	Sequence 15, Appl
30	36	100.0	36	3	US-09-315-304B-497	Sequence 497, App
31	36	100.0	36	3	US-09-315-304B-498	Sequence 498, App
32	36	100.0	36	3	US-09-315-304B-603	Sequence 603, App
33	36	100.0	36	3	US-09-315-304B-630	Sequence 630, App
34	36	100.0	36	3	US-09-315-304B-631	Sequence 631, App
35	36	100.0	36	3	US-09-315-304B-705	Sequence 705, App
36	36	100.0	36	3	US-09-315-304B-834	Sequence 834, App
37	36	100.0	36	3	US-09-315-304B-1076	Sequence 1076, App
38	36	100.0	36	3	US-09-315-304B-1121	Sequence 1121, App
39	36	100.0	36	3	US-09-315-304B-1161	Sequence 1161, App
40	36	100.0	36	3	US-09-315-304B-1469	Sequence 1469, App
41	36	100.0	36	3	US-09-315-304B-1470	Sequence 1470, App
42	36	100.0	36	3	US-09-315-304B-1486	Sequence 1486, App
43	36	100.0	36	4	US-08-255-208A-1	Sequence 1, Appl
44	36	100.0	36	4	US-08-973-952-1	Sequence 1, Appl
45	36	100.0	36	4	US-08-470-896-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-073-028-1
Sequence 1, Application US/08073028
Patent No. 5464933
GENERAL INFORMATION:
APPLICANT: Biologues, Dani P.
APPLICANT: Matthews, Thomas J.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,028
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8644/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-073-028-1
Query Match 100.0%; Score 36; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 YTSLSHSLIESQNOQEKNEQLELDKMSLWNMF 36
|||||

Db 1 YTSLSHLSIESONQOEKNEQELLELDKMSLWNMF 36

RESULT 2
US-08-486-099-1
; Sequence 1, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486, 099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-099-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKMSLWNMF 36
Db 1 YTSLSHLSIESONQOEKNEQELLELDKMSLWNMF 36

RESULT 3
US-09-071-877-1
; Sequence 1, Application US/09071877
; Patent No. 6015881
; GENERAL INFORMATION:
; APPLICANT: Kang, Myung-Chol
; APPLICANT: Bray, Brian
; APPLICANT: Lichey, Maynard
; APPLICANT: Mader, Catherine
; APPLICANT: Merutka, Gene
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS
; FILE REFERENCE: 7872-050

; CURRENT APPLICATION NUMBER: US/09/071,877
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-071-877-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKMSLWNMF 36
Db 1 YTSLSHLSIESONQOEKNEQELLELDKMSLWNMF 36

RESULT 4
US-08-360-107A-1
; Sequence 1, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-360-107A-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKMSLWNMF 36

Db 1 YTSLSHSLIBESQOQKNEQLELDKMSLWVWF 36

RESULT 5
US-08-484-223B-1

Sequence 1, Application US/08484223B
Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-484-223B-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLSHSLIBESQOQKNEQLELDKMSLWVWF 36

RESULT 6
US-08-919-597-1

Sequence 1, Application US/08919597

Patent No. 6034265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,896

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-919-597-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLSHSLIBESQOQKNEQLELDKMSLWVWF 36

RESULT 7
US-08-475-668A-1

Sequence 1, Application US/08475668A

Patent No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

US-08-475-668A-1

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-475-668A-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDKVASLWNMF 36
Db 1 YTSLSHLSIESQNOQEKNEQELLEDKVASLWNMF 36

RESULT 8
US-08-485-551A-1
Sequence 1, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDKVASLWNMF 36
Db 1 YTSLSHLSIESQNOQEKNEQELLEDKVASLWNMF 36

RESULT 9
US-08-471-913A-1
Sequence 1, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDKVASLWNMF 36
Db 1 YTSLSHLSIESQNOQEKNEQELLEDKVASLWNMF 36

RESULT 10
US-08-554-616-1
Sequence 1, Application US/08554616
Patent No. 6133418
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,028
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36
DB 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 11
US-08-485-264A-1
Sequence 1, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-264A-1

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36
DB 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 12
US-09-082-279B-15
Sequence 15, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Lambert, Dennis
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-15

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36

RESULT 13

US-09-082-279B-497
Sequence 497, Application US/09082279B

Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 497
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-497

Query Match

100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36
Db 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36

RESULT 14

US-09-082-279B-498
Sequence 498, Application US/09082279B

Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 498
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-498

Query Match

100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36
Db 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36

RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 603
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-603

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36
Db 1 YTSLSHSLIESONQOEKNEQELLELDKMASLWNMF 36

Search completed: September 20, 2005, 19:59:37
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2005, 19:52:21 ; Search time 168 Seconds
(without alignments)
86.770 Million cell updates/sec

Title: US-09-809-060A-1
Perfect score: 36
Sequence: 1 YTSLSHSLIESQNOEKNEQELLEDKMASLWNMF 36

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1812044 seqs, 404927589 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	36	100.0	36	9	US-09-809-060-1
2	36	100.0	36	9	US-09-809-060-85
3	36	100.0	36	9	US-09-796-202-10
4	36	100.0	36	9	US-09-960-717-2
5	36	100.0	36	9	US-09-779-451-5
6	36	100.0	36	9	US-09-834-628-1
7	36	100.0	36	9	US-09-828-615-1
8	36	100.0	36	9	US-09-854-816-1
9	36	100.0	36	9	US-09-854-816-108
10	36	100.0	36	9	US-09-874-475-16
11	36	100.0	36	10	US-09-493-346-1

12	36	100.0	36	14	US-10-116-797-1	Sequence 1, Appl1
13	36	100.0	36	14	US-10-252-136-1	Sequence 1, Appl1
14	36	100.0	36	14	US-10-158-742A-8	Sequence 8, Appl1
15	36	100.0	36	14	US-10-323-314-10	Sequence 10, Appl1
16	36	100.0	36	14	US-10-278-364A-7	Sequence 7, Appl1
17	36	100.0	36	14	US-10-351-641-15	Sequence 15, Appl1
18	36	100.0	36	14	US-10-351-641-497	Sequence 497, App
19	36	100.0	36	14	US-10-351-641-498	Sequence 498, App
20	36	100.0	36	14	US-10-351-641-603	Sequence 603, App
21	36	100.0	36	14	US-10-351-641-630	Sequence 630, App
22	36	100.0	36	14	US-10-351-641-631	Sequence 631, App
23	36	100.0	36	14	US-10-351-641-705	Sequence 705, App
24	36	100.0	36	14	US-10-351-641-834	Sequence 834, App
25	36	100.0	36	14	US-10-351-641-1076	Sequence 1076, App
26	36	100.0	36	14	US-10-351-641-1121	Sequence 1121, App
27	36	100.0	36	14	US-10-351-641-1161	Sequence 1161, App
28	36	100.0	36	14	US-10-351-641-1469	Sequence 1469, App
29	36	100.0	36	14	US-10-351-641-1470	Sequence 1470, App
30	36	100.0	36	14	US-10-351-641-1486	Sequence 1486, App
31	36	100.0	36	15	US-10-005-305-34	Sequence 34, Appl1
32	36	100.0	36	15	US-10-005-305-67	Sequence 67, Appl1
33	36	100.0	36	15	US-10-005-305-197	Sequence 197, App
34	36	100.0	36	15	US-10-378-094-17	Sequence 17, Appl1
35	36	100.0	36	15	US-10-420-194-1233	Sequence 1233, App
36	36	100.0	36	15	US-10-231-494-14	Sequence 14, Appl1
37	36	100.0	36	15	US-10-267-682-1	Sequence 1, Appl1
38	36	100.0	36	15	US-10-623-873-1	Sequence 1, Appl1
39	36	100.0	36	15	US-10-267-748-1	Sequence 1, Appl1
40	36	100.0	36	15	US-10-681-879-1	Sequence 1, Appl1
41	36	100.0	36	15	US-10-663-589-4	Sequence 4, Appl1
42	36	100.0	36	15	US-10-469-199-9	Sequence 9, Appl1
43	36	100.0	36	16	US-10-625-033-1	Sequence 1, Appl1
44	36	100.0	36	16	US-10-164-290A-16	Sequence 16, Appl1
45	36	100.0	36	16	US-10-671-282-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-809-060-1
; Sequence 1, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: wild, Carl T.
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809, 060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-1

Query Match 100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLSHSLIESQNOEKNEQELLEDKMASLWNMF 36
DB 1 YTSLSHSLIESQNOEKNEQELLEDKMASLWNMF 36
RESULT 2
US-09-809-060-85

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; Sequence 85, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Generating Immungene that Elicit
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/809,060
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/189,981
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-809-060-85
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Query Match          100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 YTSLSHSLIEESQNOEKNEQELLEDKVASLWNMF 36
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RESULT 3
US-09-796-202-10
; Sequence 10, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olsom, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/3PM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: T-20
US-09-796-202-10
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Query Match          100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 YTSLSHSLIEESQNOEKNEQELLEDKVASLWNMF 36
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RESULT 4
US-09-960-717-2
; Sequence 2, Application US/09960717
; Publication No. US20020086283A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: PATEL, DHAVALKUMAR D.
; APPLICANT: ALAM, MUNIR
; APPLICANT: LIAO, HUA-XIN
; TITLE OF INVENTION: IMMUNOGEN
; FILE REFERENCE: 1579-599
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; CURRENT APPLICATION NUMBER: US/09/960,717
; CURRENT FILING DATE: 2001-09-16
; PRIOR APPLICATION NUMBER: 60/234,327
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/285,173
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/323,697
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/323,702
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human Immunodeficiency Virus
US-09-960-717-2
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Query Match          100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 YTSLSHSLIEESQNOEKNEQELLEDKVASLWNMF 36
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US-09-779-451-5
; Sequence 5, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-5
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Query Match          100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 YTSLSHSLIEESQNOEKNEQELLEDKVASLWNMF 36
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RESULT 6
US-09-834-628-1
; Sequence 1, Application US/09834628
; Patent No. US20020119922A1
; GENERAL INFORMATION:
; APPLICANT: YU, YEON GYU
; APPLICANT: KIM, KEY-SUN
; APPLICANT: JIN, BONG-SUK
; TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION
; FILE REFERENCE: 05823.0198-0000
; CURRENT APPLICATION NUMBER: US/09/834,628
; CURRENT FILING DATE: 2001-04-16
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PRIOR APPLICATION NUMBER: KR 00-65664
PRIOR FILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
OTHER INFORMATION: DP178
US-09-834-628-1

Query Match 100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 7
US-09-828-615-1
Sequence 1, Application US/09828615
Publication No. US20020146415A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672
CURRENT APPLICATION NUMBER: US/09/828, 615
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-615-1

Query Match 100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 8
US-09-854-816-1
Sequence 1, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854, 816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965, 056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-854-816-1

Query Match 100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNMF 36
Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 9
US-09-854-816-108
Sequence 108, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854, 816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965, 056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-854-816-108
SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Query Match 100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36
DB 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36

RESULT 10
US-09-874-475-16
Sequence 16, Application US/09874475
Publication No. US20020182592A1
GENERAL INFORMATION:
APPLICANT: Petropoulos, Christos J.
APPLICANT: Parkin, Neil T.
APPLICANT: Whitcomb, Jeanette
APPLICANT: Huang, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECEPTOR
TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS
FILE REFERENCE: 2793/6516
CURRENT APPLICATION NUMBER: US/09/874,475
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 36
TYPE: PRT
ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match 100.0%; Score 36; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36
DB 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36

RESULT 11
US-09-493-346-1
Sequence 1, Application US/09493346
Publication No. US20030082185A1
GENERAL INFORMATION:
APPLICANT: Olson, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
TITLE OF INVENTION: Infection
FILE REFERENCE: 61009
CURRENT APPLICATION NUMBER: US/09/493,346
CURRENT FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide
US-09-493-346-1

Query Match 100.0%; Score 36; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36
DB 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36

RESULT 12
US-10-116-797-1
Sequence 1, Application US/10116797
Publication No. US20030044411A1
GENERAL INFORMATION:
APPLICANT: Olsen, William C.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
FILE REFERENCE: 64672-A
CURRENT APPLICATION NUMBER: US/10/116,797
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-797-1

Query Match 100.0%; Score 36; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36
DB 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36

RESULT 13
US-10-252-136-1
Sequence 1, Application US/10252136
Publication No. US2003010398A1
GENERAL INFORMATION:
APPLICANT: Johnson, M. Ross
APPLICANT: Lambert, Dennis M.
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
TITLE OF INVENTION: VIRAL INFECTIONS
TITLE OF INVENTION: USING COMBINATORY THERAPY
FILE REFERENCE: 7872-036
CURRENT APPLICATION NUMBER: US/10/252,136
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/08/973,952
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 36
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-252-136-1

Query Match 100.0%; Score 36; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36
DB 1 YTSLSLIESONQOEKNEQELLEDKWSLWNMF 36

RESULT 14
US-10-158-742A-8
Sequence 8, Application US/10158742A
Publication No. US20030104581A1

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; GENERAL INFORMATION:
; APPLICANT: Hoeess, Eva
; APPLICANT: Meier, Thomas
; APPLICANT: Pestlin, Gabriele
; APPLICANT: Popp, Friedrich
; APPLICANT: Reichert, Klaus
; APPLICANT: Schmuck, Rainer
; APPLICANT: Schneider, Bernd
; APPLICANT: Seidel, Christoph
; APPLICANT: Tischler, Wilhelm
; TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM
; TITLE OF INVENTION: INCLUSION ANTIBODIES
; FILE REFERENCE: 20904
; CURRENT APPLICATION NUMBER: US/10/158, 742A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: EP 01114497.9
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE:
; SEQ ID NO: 8
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide T680
US-10-158-742A-8

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Query Match          100.0%; Score 36; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 YTSLIHSLIESQNOQEKNEQELLELDKMASLWNMF 36
DB      1 YTSLIHSLIESQNOQEKNEQELLELDKMASLWNMF 36

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RESULT 15
US-10-323-314-10
; Sequence 10, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: T-20
US-10-323-314-10

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Query Match          100.0%; Score 36; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 YTSLIHSLIESQNOQEKNEQELLELDKMASLWNMF 36
DB      1 YTSLIHSLIESQNOQEKNEQELLELDKMASLWNMF 36

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Search completed: September 20, 2005, 20:02:32
Job time : 169 secs

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